

GenCore version 4.5
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3M protein - protein search, using sw model

Run on: July 15, 2002, 11:03:27 : Search time 20.17 sec
(without alignments)
13,125 Matches, 511 of interest

Hit no: 05-09-719-053A-4
Percent score: 52
Sequence: 1 MEPLAGPVT 11

Scoring table:
EloSim62
Gap 10.0, GapExt 0.5

Searched: 241628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 76679

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued_Patents_AA*
1: 7-162-2 P 0411-2133 5A-7098 pep*
2: 7-162-2 P 0411-2133 5A-7098 pep*
3: 7-162-2 P 0411-2133 5A-7098 pep*
4: 7-162-2 P 0411-2133 5A-7098 pep*
5: 7-162-2 P 0411-2133 5A-7098 pep*
6: 7-162-2 P 0411-2133 5A-7098 pep*
7: 7-162-2 P 0411-2133 5A-7098 pep*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	92.3	11	2	US-09-090-567-4
2	25	46.1	10	1	US-08-313-075A-26
3	24	46.2	9	2	US-08-502-046-14
4	23	44.2	9	4	US-07-861-4580-125
5	23	44.2	11	1	US-07-912-900-2
6	23	44.2	11	1	US-08-285-409-2
7	23	44.2	11	2	US-08-502-046-14
8	22	42.3	9	2	US-08-203-662-2
9	22	42.3	11	1	US-07-912-900-15
10	22	42.3	11	1	US-07-912-900-14
11	22	42.3	11	1	US-07-912-900-15
12	22	42.3	11	1	US-08-285-409-2
13	22	42.3	11	1	US-08-285-409-14
14	22	42.3	11	1	US-08-285-409-14
15	22	42.3	11	1	US-08-285-409-14
16	22	42.3	11	1	US-08-313-075A-12
17	22	42.3	11	1	US-08-313-075A-13
18	22	42.3	11	1	US-08-313-075A-14
19	22	42.3	11	2	US-08-502-046-14
20	22	42.3	11	2	US-08-502-046-14
21	21	41.4	8	4	US-08-444-818-679
22	21	41.4	8	4	US-08-444-818-680
23	21	41.4	8	4	US-08-444-818-681
24	21	40.4	8	4	US-08-444-818-682
25	21	40.4	9	1	US-08-207-169A-10
26	21	40.4	9	1	US-08-467-083-8
27	21	40.4	9	1	US-08-414-417B-8

28	21	40.4	9	2	US-08-485-448A-8	Sequence 8, App1
29	21	40.4	9	2	US-08-468-545B-8	Sequence 8, App1
30	21	40.4	9	3	US-08-466-680B-8	Sequence 8, App1
31	21	40.4	10	4	US-09-139-802-41	Sequence 41, App1
32	21	40.4	10	6	5210075-18	Patent No. 5210075
33	20	38.5	7	1	US-08-487-890A-78	Sequence 78, App1
34	20	38.5	7	2	US-08-478-445-78	Sequence 78, App1
35	20	38.5	7	2	US-08-372-452-78	Sequence 78, App1
36	20	38.5	7	2	US-08-478-473-78	Sequence 78, App1
37	20	38.5	7	3	US-08-478-473-78	Sequence 78, App1
38	20	38.5	7	3	US-08-483-577A-78	Sequence 78, App1
39	20	38.5	7	4	US-08-897-448-78	Sequence 78, App1
40	20	38.5	7	4	US-08-637-664-78	Sequence 78, App1
41	20	38.5	8	1	US-08-266-514-17	Sequence 17, App1
42	20	38.5	8	1	US-08-214-897A-2	Sequence 2, App1
43	20	38.5	8	2	US-08-664-604-17	Sequence 17, App1
44	20	38.5	8	2	US-08-726-406A-164	Sequence 164, App1
45	20	38.5	8	2	US-08-795-722-18	Sequence 18, App1

ALIGNMENTS

RESULT 1
US-09-090-567-4
Sequence 4, Application US/06/090567
Patent No. 5989549
GENERAL INFORMATION:
APPLICANT: Sullivan, Robert
ATTORNEY: Brub, Bruno
INVENTOR: Brub, Bruno
TITLE OF INVENTION: Amino Acid Specific Protein And
METHOD OF SYNTHESIS
ADDRESS: Swabey Hallway Renault
STREET: 1600 - 1961 McGill College
CITY: Montreal
STATE: QC
COUNTRY: Canada
ZIP: H3A 2Y4
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows
SOFTWARE: FASTSPD for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 35/57/090,567
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Kevin P
REGISTRATION NUMBER: 26,674
FIRM: N.E.L.E.-7611 N.E.L.E. 17045-2705 13200
TELEPHONE: 514 845 7126
TELEFAX: 514-288-8389
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
SYNANALYSIS: single
TOPOLOGY: linear
MOTIF TYPE: peptide
US-09-090-567-4

Query Match 92.3% Score 48 DB 2 Length 11

Post Local Similarity: 100.0%; Prod. No. 0.000267
Matches: 10; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0

QY 1 BLPLAGRRV 10
11111111
ID 1 BLPLAGRRV 10

RESULT 2

US-09-719-053a-4
Sequence 26, Application US/070707A
Patent No. 5689870
GENERAL INFORMATION:
APPLICANT: Johnson, Timothy A.
APPLICANT: Coriush, Pamela C.
APPLICANT: Tabor, Yoshiko
TITLE OF INVENTION: GENE EXPRESSION INDICATING FLAVINOL
TITLE OF INVENTION: FAIRWAY ENZYME AND GENE IDENTIFICATION
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIA TYPE: floppy disk
SOFTWARE: IBM PC compatible
OF INVENTION: 10/15/93
CURRENT APPLICATION DATA:
FILING DATE: 07/08/93, Version #1.25
APPLICATION NUMBER: US/93/03707A
FILING DATE: 30 Nov 1994
CLASSIFICATION: B01
PRIORITY INFORMATION:
APPLICATION NUMBER: At. 1538,792
FILING DATE: 27 MAR 1992
PRIORITY INFORMATION:
APPLICATION NUMBER: At. 15,987,932
FILING DATE: 07 JAN 1994
PRIORITY INFORMATION:
APPLICATION NUMBER:
FILING DATE: 25 MAR 1994
ATTORNEY/AGENT INFORMATION:
NAME: DeGiglio, Frank S.
REGISTRATION NUMBER: 41,846
REFERENCE/BOOK NUMBER: 44-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4444
TELEFAX: (516) 742-4466
TITLE: 261 901 SANS DR 251
INFORMATION FOR SEQ ID NO: 251
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
Topology: linear
MODIFIABLE TYPE: protein
US-09-719-053a-4

Query Match: 48.4%; Score 25; ID 1; Length 10
Post Local Similarity: 71.4%; Prod. No. 211
Matches: 5; Conservative: 1; Mismatches: 1; Indels: 0; Gaps: 0

QY 4 BLPLAGRRV 10
11111111
ID 2 BLPLAGRRV 10

RESULT 4
US-09-719-053a-4
Sequence 26, Application US/070707A

Patent No. 5646715
GENERAL INFORMATION:
APPLICANT: PORCELL, Damian F. J.
APPLICANT: RUSSELL, Sarah M.
APPLICANT: BRENNIE, Ian F. O.
TITLE OF INVENTION: C245 VARIANTS
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIA TYPE: 3.5 inch disk
SOFTWARE: IBM PC compatible
OF INVENTION: 10/15/93
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/93/03707A
FILING DATE: 07/08/93, Version #1.25
APPLICATION NUMBER: US/93/03707A
FILING DATE: 30 Nov 1994
CLASSIFICATION: B01
PRIORITY INFORMATION:
APPLICATION NUMBER: At. 1538,792
FILING DATE: 27 MAR 1992
PRIORITY INFORMATION:
APPLICATION NUMBER: At. 15,987,932
FILING DATE: 07 JAN 1994
PRIORITY INFORMATION:
APPLICATION NUMBER:
FILING DATE: 25 MAR 1994
ATTORNEY/AGENT INFORMATION:
NAME: DeGiglio, Frank S.
REGISTRATION NUMBER: 41,846
REFERENCE/BOOK NUMBER: 44-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4444
TELEFAX: (516) 742-4466
TITLE: 261 901 SANS DR 251
INFORMATION FOR SEQ ID NO: 251
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
Topology: linear
MODIFIABLE TYPE: protein
US-09-719-053a-4

Query Match: 48.2%; Score 24; ID 2; Length 9
Post Local Similarity: 70.0%; Prod. No. 1.70e-05
Matches: 4; Conservative: 2; Mismatches: 2; Indels: 0; Gaps: 0

QY 2 BLPLAGRRV 9
11111111
ID 1 BLPLAGRRV 8

RESULT 4
US-07-861-4580-125
Sequence 125, Application US/070414580
Patent No. 6232061
GENERAL INFORMATION:
APPLICANT: Marchionni, Mark Andrew
APPLICANT: Johnson, Carl D.
TITLE OF INVENTION: BIOGENIC CYCLING
NUMBER OF SEQUENCES: 142
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
CITY: Washington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:

MEDIAN TYPE: 2.5" D. OBJECT: 1.44 MB
 COMPUTER: IBM PC/XT Model 586 at 66MHz
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 05/07/051.4560
 FILING DATE: 04/01/92
 CLASSIFICATION: 485
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark Paul
 REGISTRATION NUMBER: 40,162
 PER-FILE # SET #7M-04 150071001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELETYPE: 200154
 INFORMATION FOR SEQ ID #1: 125;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9
 TYPE: amino acid
 TOPOLOGY: linear
 US-07-061-459C-125

Query Match 44.2% Score 24 DB 4 Length 11
 Host Local Similarity 83.4% Ident. No. 170-05
 Matches 5 Conservative 0 Mismatches 1 Indels 0

QY 3 LEPLGR 9
 11 11
 1b 4 LEPLGR 3

RESULT 5
 US-07-912-990-2
 Sequence 2: Application US/07912900
 Patent No. 5449125
 GENERAL INFORMATION:
 APPLICANT: Holton, Timothy A.
 APPLICANT: Cornish, Edwina G.
 APPLICANT: Kovacic, Filipa
 APPLICANT: Tanaka, Yoshikazu
 TITLE OF INVENTION: GENETIC SEQUENCES ENCODING TAY A 11
 TITLE OF INVENTION: PATHWAY DEVICES AND THEIR THREE-D
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 11540
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 05/07/912.990
 FILING DATE: 10/20/91
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Dittiglio, Frank S.
 REGISTRATION NUMBER: 31,446
 PER-FILE # SET #7M-04 150071001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4344
 TELEFAX: (516) 742-4366
 TELETYPE: 240 901 SANS DR

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MULTIPLE TYPE: peptide
 US-07-912-900-2

Query Match 44.2% Score 24 DB 1 Length 11
 Host Local Similarity 80.0% Ident. No. 64
 Matches 4 Conservative 1 Mismatches 0 Indels 0

QY 5 AGRV 10
 11 11
 1b 4 AGRV 8

RESULT 6
 US-09-285-309-2
 Sequence 2: Application US/08285309
 Patent No. 5569832
 GENERAL INFORMATION:
 APPLICANT: Holton, Timothy A.
 APPLICANT: Cornish, Edwina G.
 APPLICANT: Kovacic, Filipa
 APPLICANT: Tanaka, Yoshikazu
 TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'
 TITLE OF INVENTION: HYDROLYASE AND USES
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 11540
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 05/08/285.309
 FILING DATE: 03 AUG-1994
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Dittiglio, Frank S.
 REGISTRATION NUMBER: 31,446
 PER-FILE # SET #7M-04 150071001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4344
 TELEFAX: (516) 742-4366
 TELETYPE: 240 901 SANS DR
 MULTIPLE TYPE: peptide
 US-08-285-309-2

Query Match 44.2% Score 24 DB 1 Length 11
 Host Local Similarity 80.0% Ident. No. 64
 Matches 4 Conservative 1 Mismatches 0 Indels 0

QY 6 AGRV 10
 11 11
 1b 4 AGRV 8

RESULT 7

US-08-502-046-2
Sequence 2: Application US/08-02046
Patent No. 5961487
GENERAL INFORMATION:
APPLICANT: Bolton, Timothy A.
APPLICANT: Cornish, Edwin C.
APPLICANT: Kovacic, Philip A.
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 5'-
TITLE OF INVENTION: HYDROXYLASE AND USES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-502-046
FILING DATE: 14 JUL-1996
CLASSIFICATION: 800
PR OR APPLICATION DATA:
APPLICATION NUMBER: 08/206,409
FILING DATE: 03 AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: DigiGlio, Frank S.
REGISTRATION NUMBER: 41,446
REFERENCE/EXETER NUMBER: 36332
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4444
TELEFAX: (516) 742-4446
TELEX: 240 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-502-046-2

Query Match

Best Local Similarity: 44.2% Score 23 DB 2: Length 11
Matches: 4: Conservative 1: Mismatches 0: Indels 0: Gaps 0

QY 5 ARRY 10
1111

ID 4 ARRY 8

RESULT 8

US-08-203-66-2
Sequence 2: Application US/08203662
Patent No. 5869278
GENERAL INFORMATION:
APPLICANT: Guido Grandi
APPLICANT: Giuliano Galini
TITLE OF INVENTION: FREES FOR THE PREPARATION OF MATURE
TITLE OF INVENTION: HUMAN GROWTH HORMONE BY ENZYMATIC WITH CATALYTIC A GARDEN CITY
TITLE OF INVENTION: WITH IMMEDIATE FACTOR A
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

ADDRESSEE: Rogers & Wells LLP
STREET: 200 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10166-0154

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.40 (1997)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/203,662
FILING DATE: February 20, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Roux, Philip E.
REGISTRATION NUMBER: 31,296
REFERENCE/EXETER NUMBER: 254,177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 878-8375
TELEFAX: (212) 878-8000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-203-66-2

Query Match

Best Local Similarity: 42.4% Score 23 DB 2: Length 9
Matches: 4: Conservative 1: Mismatches 2: Indels 0: Gaps 0

QY 2 ELIAGR 8
1111

ID 3 ELIAGR 9

RESULT 9

US-07-912-900-13
Sequence 13: Application US/07912900
Patent No. 5349125
GENERAL INFORMATION:
APPLICANT: Bolton, Timothy A.
APPLICANT: Cornish, Edwin C.
APPLICANT: Kovacic, Philip A.
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
TITLE OF INVENTION: UTRINARY ENZYMS AND USES THEREOF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/912,900
FILING DATE: 19920713
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: DigiGlio, Frank S.
REGISTRATION NUMBER: 41,446
REFERENCE/EXETER NUMBER: 36332

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: (23) 901 SANS DR

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-912-900-13

Query Match:

42.38; Score 22; DB 1; Length 11;

Post Local Similarity 57.18; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0;

US-07-912-900-13

4 FLARRV 9

1 I I I I

2 FGAGRR 7

US-07-912-900-14

Sequence 14, Application US/07912900

Patent No. 5349125

GENERAL INFORMATION:

APPLICANT: Holtan, Timothy A.

APPLICANT: Kornish, Edwina C.

APPLICANT: Kovacic, Filipa

APPLICANT: Tanaka, Yoshikazu

APPLICANT: Ioster, Diane R.

TITLE OF INVENTION: CHITTO SEQUENCES ENCODING FLAVIN IN

TITLE OF INVENTION: PATHWAY ENZYMS AND USES THEREOF

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: U.S.A.

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 05/07912,900

FILING DATE: 19920713

CLASSIFICATION: B01

ATTORNEY/AGENT INFORMATION:

NAME: Digitalio, Frank S.

REGISTRATION NUMBER: 41,446

REFERENCE/BOOK NUMBER: 8633

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 240 901 SANS DR

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-912-900-14

Query Match:

42.38; Score 22; DB 1; Length 11;

Post Local Similarity 57.18; Pred. No. 1.1e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0;

US-07-912-900-14

RESULT 11

US-07-912-900-15

Sequence 15, Application US/07912900

Patent No. 5349125

GENERAL INFORMATION:

APPLICANT: Holtan, Timothy A.

APPLICANT: Kornish, Edwina C.

APPLICANT: Kovacic, Filipa

APPLICANT: Tanaka, Yoshikazu

APPLICANT: Ioster, Diane R.

TITLE OF INVENTION: CHITTO SEQUENCES ENCODING FLAVIN IN

TITLE OF INVENTION: PATHWAY ENZYMS AND USES THEREOF

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: U.S.A.

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 05/07912,900

FILING DATE: 19920713

CLASSIFICATION: B01

ATTORNEY/AGENT INFORMATION:

NAME: Digitalio, Frank S.

REGISTRATION NUMBER: 41,446

REFERENCE/BOOK NUMBER: 8633

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 240 901 SANS DR

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-07-912-900-15

Query Match:

42.38; Score 22; DB 1; Length 11;

Post Local Similarity 57.18; Pred. No. 1.1e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0;

US-07-912-900-15

4 FLARRV 10

1 I I I I

2 FGAGRR 8

US-07-912-900-13

Sequence 13, Application US/07912900

Patent No. 5349125

GENERAL INFORMATION:

APPLICANT: Holtan, Timothy A.

APPLICANT: Kornish, Edwina C.

APPLICANT: Kovacic, Filipa

APPLICANT: Tanaka, Yoshikazu

APPLICANT: Ioster, Diane R.

TITLE OF INVENTION: CHITTO SEQUENCES ENCODING FLAVIN IN

TITLE OF INVENTION: PATHWAY ENZYMS AND USES THEREOF

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: U.S.A.

1 TITLE OF INVENTION: HYPERXYLASE AND USES
 2 NUMBER OF SEQUENCE: 29
 3 CORRESPONDENCE ADDRESS:
 4 ADDRESSEE: Scully, Scott, Murphy & Prosser
 5 STREET: 400 Garden City Plaza
 6 CITY: Garden City
 7 STATE: New York
 8 COUNTRY: U.S.A.
 9 ZIP: 11530
 10 COMPUTER READABLE FORM:
 11 MEDIUM TYPE: Floppy disk
 12 COMPUTER: IBM PC compatible
 13 OPERATING SYSTEM: PC DOS/MS DOS
 14 SOFTWARE: Patent In Release #1.0, Version #1.25
 15 CURRENT APPLICATION DATA:
 16 APPLICATION NUMBER: US/08/285,309
 17 FILING DATE: 03 AUG 1994
 18 CLASSIFICATION: B00
 19 ATTORNEY/AGENT INFORMATION:
 20 NAME: Diodato, Frank S.
 21 REGISTRATION NUMBER: 31,346
 22 REFERENCE/DOCKET NUMBER: 86432
 23 TELECOMMUNICATION INFORMATION:
 24 TELEPHONE: (516) 742-4444
 25 TELEFAX: (516) 742-4466
 26 TELEX: 230 901 SANS UR
 27 INFORMATION FOR SEQ ID NO: 13
 28 SEQUENCE CHARACTERISTICS:
 29 LENGTH: 11 amino acids
 30 TYPE: amino acid
 31 STRANDEDNESS: single
 32 TOPOLOGY: linear
 33 MOLECULE TYPE: peptide
 34 US-08-285-309-13
 35
 36 Query Match 42.1% Score 23; ID: 1; Length: 11
 37 Best Local Similarity: 82.4% Prod. No. 1,10-02;
 38 Matches: 5; Conservative: 0; Mismatches: 1; Gaps: 0;
 39
 40 QY 4 FLAGR 9
 41 1 1 1 1
 42 DB 2 FLAGR 7
 43
 44 RESULT 14
 45 US-08-285-309-14
 46 Sequence 14, Application US/08/285,309
 47 Patent No. 5569842
 48 GENERAL INFORMATION:
 49 APPLICANT: Holton, Timothy A.
 50 APPLICANT: Cornish, Edwin G.
 51 APPLICANT: Kovacic, Filipa
 52 APPLICANT: Tanaka, Yoshikazu
 53 APPLICANT: Lester, Diane R.
 54 TITLE OF INVENTION: GRAFTING COMPOUNDING ENDOTIN A 3.5
 55 NUMBER OF SEQUENCE: 29
 56 TITLE OF INVENTION: HYPERXYLASE AND USES
 57 CORRESPONDENCE ADDRESS:
 58 ADDRESSEE: Scully, Scott, Murphy & Prosser
 59 STREET: 400 Garden City Plaza
 60 CITY: Garden City
 61 STATE: New York
 62 COUNTRY: U.S.A.
 63 ZIP: 11530
 64 COMPUTER READABLE FORM:
 65 MEDIUM TYPE: Floppy disk
 66 COMPUTER: IBM PC compatible
 67 OPERATING SYSTEM: PC DOS/MS DOS
 68 SOFTWARE: Patent In Release #1.0, Version #1.25
 69 CURRENT APPLICATION DATA:
 70 APPLICATION NUMBER: US/08/285,309
 71 FILING DATE: 03 AUG 1994
 72 CLASSIFICATION: B00
 73 ATTORNEY/AGENT INFORMATION:
 74 NAME: Diodato, Frank S.
 75 REGISTRATION NUMBER: 31,346
 76 REFERENCE/DOCKET NUMBER: 86432
 77 TELECOMMUNICATION INFORMATION:
 78 TELEPHONE: (516) 742-4444
 79 TELEFAX: (516) 742-4466
 80 TELEX: 230 901 SANS UR
 81 INFORMATION FOR SEQ ID NO: 15
 82 SEQUENCE CHARACTERISTICS:
 83 LENGTH: 15
 84 TYPE: amino acid
 85 STRANDEDNESS: single
 86 TOPOLOGY: linear
 87 MOLECULE TYPE: DNA (genomic)
 88 US-08-285-309-15

1 CLASSIFICATION: B00
 2 ATTORNEY/AGENT INFORMATION:
 3 NAME: Diodato, Frank S.
 4 REGISTRATION NUMBER: 31,346
 5 REFERENCE/DOCKET NUMBER: 86432
 6 TELECOMMUNICATION INFORMATION:
 7 TELEPHONE: (516) 742-4444
 8 TELEFAX: (516) 742-4466
 9 TELEX: 230 901 SANS UR
 10 INFORMATION FOR SEQ ID NO: 14
 11 SEQUENCE CHARACTERISTICS:
 12 LENGTH: 14
 13 TYPE: amino acid
 14 STRANDEDNESS: single
 15 TOPOLOGY: linear
 16 MOLECULE TYPE: peptide
 17 US-08-285-309-14
 18
 19 Query Match 42.1% Score 23; ID: 1; Length: 11
 20 Best Local Similarity: 57.1% Prod. No. 1,10-02;
 21 Matches: 4; Conservative: 0; Mismatches: 1; Gaps: 0;
 22
 23 QY 4 FLAGR 10
 24 1 1 1 1
 25 DB 2 FLAGR 8
 26
 27 RESULT 14
 28 US-08-285-309-15
 29 Sequence 15, Application US/08/285,309
 30 Patent No. 5569842
 31 GENERAL INFORMATION:
 32 APPLICANT: Holton, Timothy A.
 33 APPLICANT: Cornish, Edwin G.
 34 APPLICANT: Kovacic, Filipa
 35 APPLICANT: Tanaka, Yoshikazu
 36 APPLICANT: Lester, Diane R.
 37 TITLE OF INVENTION: GRAFTING COMPOUNDING ENDOTIN A 3.5
 38 NUMBER OF SEQUENCE: 29
 39 TITLE OF INVENTION: HYPERXYLASE AND USES
 40 CORRESPONDENCE ADDRESS:
 41 ADDRESSEE: Scully, Scott, Murphy & Prosser
 42 STREET: 400 Garden City Plaza
 43 CITY: Garden City
 44 STATE: New York
 45 COUNTRY: U.S.A.
 46 ZIP: 11530
 47 COMPUTER READABLE FORM:
 48 MEDIUM TYPE: Floppy disk
 49 COMPUTER: IBM PC compatible
 50 OPERATING SYSTEM: PC DOS/MS DOS
 51 SOFTWARE: Patent In Release #1.0, Version #1.25
 52 CURRENT APPLICATION DATA:
 53 APPLICATION NUMBER: US/08/285,309
 54 FILING DATE: 03 AUG 1994
 55 CLASSIFICATION: B00
 56 ATTORNEY/AGENT INFORMATION:
 57 NAME: Diodato, Frank S.
 58 REGISTRATION NUMBER: 31,346
 59 REFERENCE/DOCKET NUMBER: 86432
 60 TELECOMMUNICATION INFORMATION:
 61 TELEPHONE: (516) 742-4444
 62 TELEFAX: (516) 742-4466
 63 TELEX: 230 901 SANS UR
 64 INFORMATION FOR SEQ ID NO: 15
 65 SEQUENCE CHARACTERISTICS:
 66 LENGTH: 15
 67 TYPE: amino acid
 68 STRANDEDNESS: single
 69 TOPOLOGY: linear
 70 MOLECULE TYPE: DNA (genomic)
 71 US-08-285-309-15

Query Match 42.3% Score 22 DB 1 Length 11
 Best Local Similarity 57.1% From No. 110-02
 Matches 4, Conservative 2, Mismatches 1, Indels 0, Gaps 0

Search completed July 15, 2002 14:07:06
 Job time: 179 sec

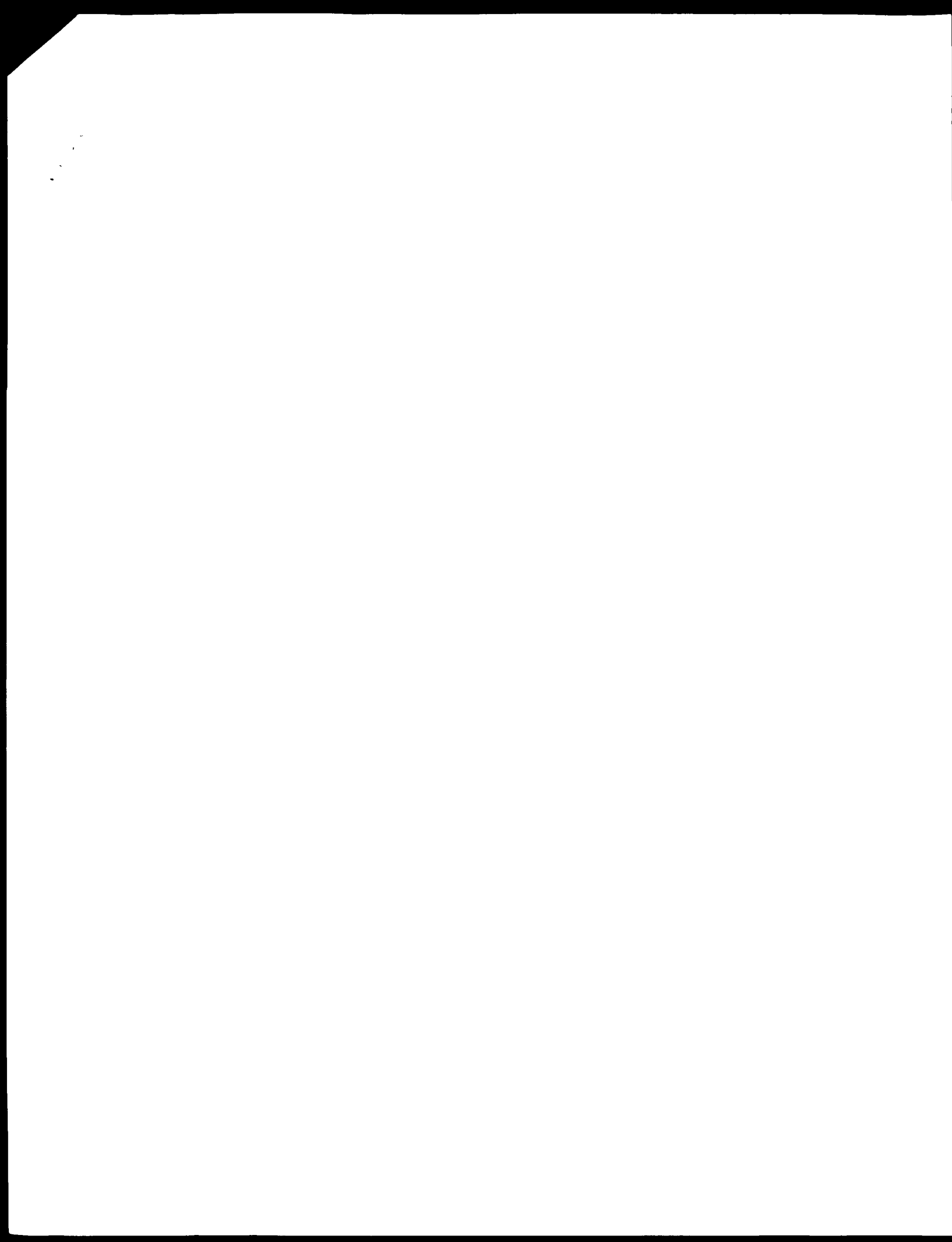
QY 4 FLAGRR 10
 1 : 111:
 DB 2 FLAGRR 8

RESULT 15

US-08-313-075A-12
 : Sequence 12, Application US/0811075A
 : Patent No. 5639870
 : GENERAL INFORMATION:
 : APPLICANT: Holton, Timothy A.
 : APPLICANT: Cornish, Edwin C.
 : APPLICANT: Tanaka, Yoshikazu
 : TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVOROL
 : TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREOF
 : NUMBER OF SEQUENCES: 58
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Seilly, Scott, Murphy & Presser
 : STREET: 400 Garden City Plaza
 : CITY: Garden City
 : STATE: New York
 : COUNTRY: U.S.A.
 : ZIP: 11540
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/313,075A
 : FILING DATE: 30-NOV-1994
 : CLASSIFICATION: 800
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: AU PL 1538/92
 : FILING DATE: 27-MAR-1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: AU PL 6698/93
 : FILING DATE: 07-JAN-1993
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: AU PL 7493/00127
 : FILING DATE: 25-MAR-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Digilio, Frank S.
 : REGISTRATION NUMBER: 31,346
 : REFERENCE/DOCKET NUMBER: 9433
 : TELEPHONE: (516) 742-4343
 : TELEFAX: (516) 742-4366
 : TELEFAX: 230 901 SANS DR
 : INFORMATION FOR SEQ ID NO: 12:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 11 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-313-075A-12

Query Match 42.3% Score 22 DB 1 Length 11
 Best Local Similarity 83.3% Prod. No. 1.1e-02
 Matches 5, conservative 0, Mismatches 1, Indels 0, Gaps 0

QY 4 FLAGRR 9
 1 : 1111
 DB 2 FLAGRR 7



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:56:12 ; Epoch: 6160 21.96 14.72 0.02

THE CONSTITUTION OF THE UNITED STATES OF AMERICA

Item:	ISS-60-S1
Partial score:	4.00

Sequence: 1 MULTICRYV. 11

Scoring table:

Method	0	1	Genex	0	5
ELFOSIM62					

Search code: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 211,222

Maximum	Seq	Let	Let
1000000000	1000000000	1000000000	1000000000

Post-Processing: Minimum Match (99%)

Max. min	Match	100
1st 1st	1st 45	

★ $A \in S$ and $A + B \in S$ imply $B \in S$.
 — S is a subalgebra of \mathcal{A} .
 — S is a σ -subalgebra of \mathcal{A} .

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1 Issue_Parents_AA.*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Rank	Pos.	Score	Qualif.	Match	Length	DR	TD	Foot	Tip	Info
1	52	100.0	244	1	US-08-762	129-1	US-08-762	1	App 1	App 1
2	48	92.4	11	2	US-09-090	567-4	US-09-090	2	App 1	App 1
3	35	67.2	577	2	US-08-766	517-12	US-08-766	2	App 1	App 1
4	32	61.5	501	1	US-08-451	715A-10	US-08-451	1	App 1	App 1
5	32	61.5	1168	1	US-08-448	170-6	US-08-448	1	App 1	App 1
6	32	61.5	1169	4	US-08-061	395-3	US-08-061	4	App 1	App 1
7	31	59.3	262	1	US-08-411	764-7	US-08-411	1	App 1	App 1
8	31	59.3	262	1	US-08-211	764-9	US-08-211	1	App 1	App 1
9	31	59.3	722	1	US-08-149	814-7	US-08-149	1	App 1	App 1
10	30	57.7	349	1	US-08-118	270-7	US-08-118	1	App 1	App 1
11	30	57.7	349	5	EC1-US93	08528-7	EC1-US93	5	App 1	App 1
12	30	57.7	350	1	US-08-204	194A-1	US-08-204	1	App 1	App 1
13	30	57.7	407	1	US-08-293	563-6	US-08-293	1	App 1	App 1
14	30	57.7	412	1	US-08-349	636-21	US-08-349	1	App 1	App 1
15	30	57.7	412	1	US-08-233	009-21	US-08-233	1	App 1	App 1
16	30	57.7	412	1	US-04-566	931-73	US-04-566	1	App 1	App 1
17	30	57.7	412	4	US-09-080	704A-21	US-09-080	4	App 1	App 1
18	30	57.7	583	4	US-08-481	190-19	US-08-481	4	App 1	App 1
19	30	57.7	583	5	EC1-US93	00869-19	EC1-US93	5	App 1	App 1
20	30	57.7	587	4	US-08-481	190-4	US-08-481	4	App 1	App 1
21	30	57.7	587	5	EC1-US93	00869-4	EC1-US93	5	App 1	App 1
22	30	57.7	588	4	US-08-481	190-16	US-08-481	4	App 1	App 1
23	30	57.7	588	5	EC1-US93	00869-16	EC1-US93	5	App 1	App 1
24	30	57.7	765	1	US-08-425	061-19	US-08-425	1	App 1	App 1
25	30	57.7	765	2	US-08-825	886-19	US-08-825	2	App 1	App 1
26	30	57.7	900	1	US-08-425	061-20	US-08-425	1	App 1	App 1
27	30	57.7	900	2	US-08-425	886-26	US-08-425	2	App 1	App 1

28	30	57.7	914	1	US-08-4825-061-21	Sequence 21, Appl
29	30	57.7	914	2	US-08-4825-061-21	Sequence 21, Appl
29	30	57.7	1202	1	US-08-4825-061-22	Sequence 22, Appl
29	30	57.7	1202	2	US-08-4825-061-22	Sequence 22, Appl
32	30	57.7	1363	1	US-08-4825-061-24	Sequence 23, Appl
32	30	57.7	1363	2	US-08-4825-061-24	Sequence 23, Appl
34	30	57.7	1462	1	US-07-7922-600-31	Sequence 31, Appl
34	30	57.7	1462	2	US-07-7922-600-31	Sequence 31, Appl
36	30	57.7	1462	3	US-07-157-021-31	Sequence 31, Appl
36	30	57.7	1462	4	US-09-156-84-71	Sequence 31, Appl
36	30	57.7	1852	1	US-08-125-051-24	Sequence 24, Appl
36	30	57.7	1852	2	US-08-125-051-24	Sequence 24, Appl
38	30	57.7	1852	2	US-08-125-051-16	Sequence 16, Appl
39	30	57.7	1863	1	US-08-598-591-2	Sequence 2, Appl
40	30	57.7	1863	1	US-08-480-794-2	Sequence 2, Appl
41	30	57.7	1863	1	US-08-483-554-2	Sequence 2, Appl
42	30	57.7	1863	1	US-08-487-003-2	Sequence 2, Appl
42	30	57.7	1863	1	US-08-487-003-2	Sequence 2, Appl
44	30	57.7	1863	1	US-08-484-554-2	Sequence 2, Appl
45	30	57.7	1863	1	US-08-798-631-2	Sequence 2, Appl

Al.11:NMH:N1:5

Result 1

Sequence 1, Application US/08762129

GENERAL INFORMATION:

APPLICANT: Goli, Surya K.

[illegible]

Alphatech, Inc., 3174 Dorrer Avenue, San Francisco, CA 94132-1001.

OFFICE: Palo Alto

COUNTRY: U
ZIP: 94304

COPIES: 1000

COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS

DIFFERENT APPLICATION DATA.

APPLICANT'S ADDRESS: 1000 E. 12th St.,

CLASSIFICATION: 514
PREF. APPLICATION: DATA

APPLICATION NUMBER:
FILING DATE:

ACTIVITY/GOAL INFORMATION:

REF ID: A66494

TEL: 415-855-0

```

1 FILENAME: 415-847-4166
2
3 FILEX:
4

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INFORMATION FOR STUDENTS:

SELECTION CHARACTERISTICS.

TYPE: amino acid

TECHNOLOGY: I intend

1. LITERATURE: COLLEGE

155-618-762-129-1

Query Match: 100.0%; Score: 52; IP: 1; Length: 244
Best Local Similarity: 100.0%; Prod. No. 0.0012;

Matches: 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 1 MELFLAGREV 11
111111111
D0 1 MELFLAGREV 11

RESULT 2

US-09-090-667-4
Sequence 4: Application US/05060667
Patent No. 5869649
GENERAL INFORMATION:
APPLICANT: Sullivan, Robert
APPLICANT: Brub, Bruce
APPLICANT: Igar, Christine
APPLICANT: Gaudreau, Christian
TITLE OF INVENTION: Acrosomal Sperm Protein And
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swaby, Ed, Ivy Renault
STREET: 1600 - 1981 McGill College
CITY: Montreal
STATE: QC
COUNTRY: Canada
ZIP: H3A 2Y3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows
SOFTWARE: Patcom 1.0 Withbase Version 2.01
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/090-667
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Kevin B.
REGISTRATION NUMBER: 26,674
REFERENCE TO PRIOR APPLICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 514-845-7126
TELEFAX: 514-288-4486
INDEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
Topology: linear
METHOD TYPE: PopInfo
US-09-090-667-4

Query Match: 92.38, Score 487, DB 25, Length 11:

Best local similarity: 10.00% Prod. No. 0.00029

Matches: 10: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 1 MELFLAGREV 10
111111111
D0 1 MELFLAGREV 10

RESULT 3

US-08-756-417-14
Sequence 14: Application US/08756417
Patent No. 5849894
GENERAL INFORMATION:
APPLICANT: Clement, Thomas R.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Minsky, Timothy A.

APPLICANT: Stark, David M.

TITLE OF INVENTION: Improved Rhodospirillum rubrum

TITLE OF INVENTION: Type B Hydroxyalkanoate Synthase

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Burke

STREET: P.O. Box 4444

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4444

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patcom Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/756-417

FILING DATE: 25-Nov-1996

CLASSIFICATION: 5.06

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/007,694

FILING DATE: 29-Nov-1995

ATTORNEY/AGENT INFORMATION:

NAME: Falcetta, Michael L.

REGISTRATION NUMBER: 34,062

REFERENCE TO PRIOR APPLICATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 767-1440

TELEFAX: (713) 767-1440

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 572 amino acids

TYPE: amino acid

STRANDEDNESS:

Topology: linear

US 08 756-417-14

Query Match: 67.09, Score 55, DB 25, Length 572:

Best local similarity: 77.89% Prod. No. 14:

Matches: 3: Conservative 1: Mismatches 1: Indels 0: Gaps 0

QY 2 MELFLAGREV 10
111111111

D0 445 MELFLAGREV 453

RESULT 4

US-08-451-715A-10
Sequence 10: Application US/08451715A
Patent No. 5801018
GENERAL INFORMATION:
APPLICANT: Tao, Jianshi
APPLICANT: Guo, Yan
APPLICANT: Honman, Fuliha
APPLICANT: Shen, Xiaoyu
APPLICANT: Schmitt, Paul R.
TITLE OF INVENTION: B-cell-derived Antineural RNA Synthesis
TITLE OF INVENTION: Effects, Nucleic Acids and Strands Comprising Same
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millbra Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02175
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patcom Release #1.0, Version #1.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 05/08/448,715A
 FILING DATE: 26-MAY-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWN, David L.
 REGISTRATION NUMBER: 22,792
 REFERENCE/CHECK NUMBER: 67194 25
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-861-6240
 TELEFAX: 617-861-9540
 INFORMATION FOR SEQ ID NO. 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 501 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-451-715A 10

Query Match 61.5% Score 32 DB 1 Length 501
 Host Local Similarity 55.6% Pred. No. 54
 Matches 5 Conservative 2 Mismatches 1 Indels 0 Gaps 0
 QY 2 EFLPACRV 10
 ID 402 EFLPACRV 410

RESULT 5
 US-08-448-170-6
 Sequence 6, Application US/08448170
 Patent No. 5727758
 GENERAL INFORMATION:
 APPLICANT: Payne, Jewel
 APPLICANT: Gammon, David A.
 APPLICANT: Cannon, Raymond J.C.
 APPLICANT: Narva, Kenneth E.
 APPLICANT: Stelman, Steve
 TITLE OF INVENTION: No. 5727758: Bacillus thuringiensis isolate denoted
 title of invention, Bt, 195002, Active Against Bt1147022 to 1147022 and 1147022
 TITLE OF INVENTION: Encoding Lepidopteran Active Toxins
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David P. Salmankovich
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: Florida
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 05/08/448,170
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 05/08/095,952
 FILING DATE: 01-JUNE-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 05/07/759,247
 FILING DATE: 17-SEP-1993
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Salmankovich, David P.
 REGISTRATION NUMBER: 11,794
 REFERENCE/CHECK NUMBER: M/5 1020 01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (904) 475 8100

TELEFAX: (904) 472-5800
 INFORMATION FOR SEQ ID NO. 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1168 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-448-170-6
 Query Match 61.5% Score 42 DB 1 Length 1168
 Host Local Similarity 60.0% Pred. No. 144-02
 Matches 6 Conservative 2 Mismatches 2 Indels 0 Gaps 0
 QY 2 EFLPACRV 11
 ID 20 EFLPACRV 29

RESULT 6
 US-08-961-803-8
 Sequence 6, Application US/08961803
 Patent No. 6150589
 GENERAL INFORMATION:
 APPLICANT: Payne, Jewel
 APPLICANT: Gammon, David A.
 APPLICANT: Cannon, Raymond J.C.
 APPLICANT: Narva, Kenneth E.
 APPLICANT: Stelman, Steve
 TITLE OF INVENTION: No. 6150589: Bacillus thuringiensis isolate denoted
 title of invention, Bt, 195002, Active Against Bt1147022 to 1147022 and 1147022
 TITLE OF INVENTION: Encoding Lepidopteran Active Toxins
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jay M. Sanders
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: Florida
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 05/08/961,803
 FILING DATE: 31-OCT-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 05/08/095,952
 FILING DATE: 01-JUNE-1994
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 05/07/759,247
 FILING DATE: 17-SEP-1993
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 05/08/448,170
 FILING DATE: 27-MAY-1995
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Sanders, Jay M.
 REGISTRATION NUMBER: 39,355
 REFERENCE/CHECK NUMBER: M/8 1020011
 TELECOMMUNICATION INFORMATION:
 TELEFAX: (407) 372 5800
 INFORMATION FOR SEQ ID NO. 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1168 amino acids
 TYPE: amino acid

STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10017-2022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5, 1/4, 360 KB Storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/469,649
 FILING DATE: June 6, 1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Barth, Richard
 REGISTRATION NUMBER: 28,180
 REFERENCE/DOCKET NUMBER: 890578CIPD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 319-4900
 TELEFAX: (212) 319-5101
 TELEX: 236268
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 332 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-OR-469,449.2

Query Match 55.5%, Score 31, DB 1, Length 332
 Best local similarity 55.5%, Pred. No. 25,
 Matches 57 Conservative 37 Mismatches 17 Indels 0 Gaps 0

QY 3 MELLAGRVL 11
 DB 253 LRIILARRIL 261

RESULT 10
 US-08-118-270-7
 Sequence 7, Application US/08118270
 Patent No. 5508384
 GENERAL INFORMATION:
 APPLICANT: Murphy, Randall B.
 APPLICANT: Schuster, David J.
 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 TITLE OF INVENTION: PEPTIDES, AND COMPOSITIONS AND METHODS THEREOF
 NUMBER OF SEQUENCES: 348
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWN AND HELMANN
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYS.EM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08-118-270
 FILING DATE: 09-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/941,236
 FILING DATE: 10-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.
 REGISTRATION NUMBER: 34,033
 REFERENCE/DOCKET NUMBER: MURPHY 2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-747-3528

TELEX: 248633
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 349 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-119-270-7

Query Match 57.7%, Score 30, DB 1, Length 349
 Best local similarity 54.5%, Pred. No. 98,
 Matches 67 Conservative 27 Mismatches 37 Indels 0 Gaps 0

QY 1 MELLAGRVL 11
 DB 187 LRIILARRIL 197

RESULT 11
 PCT-US93-08528-7
 Sequence 7, Application PCT/US9308528
 GENERAL INFORMATION:
 APPLICANT: New York University
 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 TITLE OF INVENTION: PEPTIDES, AND COMPOSITIONS AND METHODS THEREOF
 NUMBER OF SEQUENCES: 348
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWN AND HELMANN
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/08528
 FILING DATE: 09-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/941,236
 FILING DATE: 10-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.
 REGISTRATION NUMBER: 34,033
 REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-747-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 349 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US93-08528-7

Query Match 57.7%, Score 30, DB 1, Length 349
 Best local similarity 54.5%, Pred. No. 98,
 Matches 67 Conservative 27 Mismatches 37 Indels 0 Gaps 0

QY 1 MELLAGRVL 11
 DB 187 LRIILARRIL 197

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RESULT 1 1
US 08 204-196A 1
Sequence 1: Application US/08204196A
Patent No. 5646659
GENERAL INFORMATION:
APPLICANT: PERIOD, Hiroo
APPLICANT: OGAWA, Takahito
APPLICANT: FUJII, Takao
APPLICANT: NAWAHARA, Kazuhito
TITLE OF INVENTION: DNA SEQUENCE OF HUMAN PEROXISOME
TITLE OF INVENTION: HUMAN PEROXISOME
NUMBER OF SEQUENCES: 4
CORRESPONDENT ADDRESS:
ADDRESS: Baron & Thomas
STREET: 625 Statens Lane
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patient Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 09/294 196A
FILING DATE: 01 MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/0703/01309
FILING DATE: 14 SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: FLETCHER, Richard P
REGISTRATION NUMBER: 26,382
REGISTERED: 1-857 5286 P. 311 111 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 543-0500
TELEFAX: (703) 543-1080
TELEX: 89 9124 BATO AGTN
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPLOGY: circular
MULTIPLE TYPE: DNA (genomic)
US 08 204-196A 1

Query Match 57.7% Score 30; DB 1; Length 400;
Best Local Similarity 70.0%; Prot. No. 98;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

UY 2 EPILEPTIC 11
1 111 111
DB 156 EPILEPTIC 145

RESULT 1 3
US 08 293-5646
Sequence 6: Application US/082935646
Patent No. 5616694
GENERAL INFORMATION:
APPLICANT: ROBERT, Steven M.
TITLE OF INVENTION: ADD-ADDRESSING RETICLES AND
TITLE OF INVENTION: RELATIVE RELAYEDS AND BIRTH
NUMBER OF SEQUENCES: 7
CORRESPONDENT ADDRESS:
ADDRESS: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.

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ZIP: 02110 2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskettes 1.44 Mb
COMPUTER: IBM PC/XT/AT/PS/2 or ETX
OPERATING SYSTEM: MS DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,564
FILING DATE:
CLASSIFICATION: 540
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/850,188
FILING DATE: March 31, 1992
ATTORNEY/AGENT INFORMATION:
NAME: CLERK, Paul T.
REGISTRATION NUMBER: 40,162
REGISTERED: 1-800-344-7777, 1-8001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-0070
TELEFAX: (617) 542-8946
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 407
TYPE: amino acid
STRANDEDNESS: NA
TOPLOGY: linear
US 08 293-5646

Query Match 57.7% Score 30; DB 1; Length 407;
Best Local Similarity 74.7%; Prot. No. 128 02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

UY 1 EPILEPTIC 11
1 111 111
DB 193 EPILEPTIC 203

RESULT 1 4
US 08-349-696-21
Sequence 21: Application US/08349696
Patent No. 5599471
GENERAL INFORMATION:
APPLICANT: JOHNSON, Marlene A
APPLICANT: JOHNSON, Robert G
APPLICANT: JOHNSON, Christopher J
APPLICANT: SALVATORE, Christopher A
TITLE OF INVENTION: Human Abreosine Receptors
NUMBER OF SEQUENCES: 28
CORRESPONDENT ADDRESS:
ADDRESS: Brock & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: United States
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh IIx
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/349,696
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/096,905/945
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BRODITH, Roy D.
REGISTRATION NUMBER: 60,777
REGISTERED: 1-86991A

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1 TELECOMMUNICATION INFORMATION:
 2 TELEPHONE: (908)594-4720
 3 TELEFAX: (908)594-4720
 4 INFORMATION FOR SEQ ID NO: 21:
 5 SEQUENCE CHARACTERISTICS:
 6 LENGTH: 412 amino acids
 7 TYPE: amino acid
 8 STRANDEDNESS: single
 9 TOPOLOGY: linear
 10 MULTIPLE TYPE: protein
 11 US-08 449-644-21

Query Match 57.7% Score 309 108 11 Length 412
 Best Local Similarity 54.5% Pred. No. 1,20+02
 Matches 6: Conservative 2: Mismatches 4: Indels 0: Gaps 0:

QY 1 MELFLAGRAV 11
 1 111 111
 DB 198 LRIPLAKRQI 208

RESULT 15
 US-08 244-009-21
 1 Sequence 21: Application US/08233009
 2 Patent No. 5642156
 3 GENERAL INFORMATION:
 4 APPLICANT: Jacobson, Marlene A
 5 APPLICANT: Salvatore, Christopher A
 6 TITLE OF INVENTION: INHIBITION OF ESTROGEN
 7 NUMBER OF INVENTOR: ACTIVATION THROUGH A MITOCHONDRIAL ANTAGONISM
 8 CORRESPONDENCE ADDRESS:
 9 ADDRESSEE: Merck & Co., Inc.
 10 STREET: P.O. Box 2000
 11 CITY: Rahway
 12 STATE: New Jersey
 13 COUNTRY: United States
 14 ZIP: 07065
 15 COMPUTER RELEVANT FORM:
 16 MEDIUM TYPE: floppy disk
 17 COMPUTER: IBM PC compatible
 18 OPERATING SYSTEM: PC-DOS/MS-DOS
 19 SOFTWARE: Patent In Release #1.0, Version #1.25
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/08/233,009
 22 FILING DATE: 25-APR-1994
 23 CLASSIFICATION: 424
 24 ATTORNEY/AGENT INFORMATION:
 25 NAME: Berger, Gerald H
 26 REGISTRATION NUMBER: 45,746
 27 REFERENCE CHECK NUMBER: 1219
 28 TELECOMMUNICATION INFORMATION:
 29 TELEPHONE: (908)594-4720
 30 TELEFAX: (908)594-4720
 31 INFORMATION FOR SEQ ID NO: 21:
 32 SEQUENCE CHARACTERISTICS:
 33 LENGTH: 412 amino acids
 34 TYPE: amino acid
 35 TOPOLOGY: linear
 36 MULTIPLE TYPE: protein
 37 HYDROPHILIC: NO
 38 ANTI-SENSE: NO
 39 FRAGMENT TYPE: N terminal
 40 US-08 244-009-21

1 111 111
 DB 198 LRIPLAKRQI 208

Search completed: July 15, 2002, 14:59:14
 Job time: 182 sec

Query Match 57.7% Score 309 108 11 Length 412
 Best Local Similarity 54.5% Pred. No. 1,20+02
 Matches 6: Conservative 2: Mismatches 4: Indels 0: Gaps 0:

QY 1 MELFLAGRAV 11

10

Genome version 4.5
Copyright (c) 1994 - 2000 Computer 134d.

CM Protein - protein search, using SW model

Run on: July 15, 2002, 14:17:07 : Search time: 27.02 seconds

(without alignment) 59.119 Million cell updates/sec

Title: us-09-719-053a-4

Percent score: 52

Sequence: 1 MBLFACRFL 11

Scoring table: RUSUM62

Gapop 10.0 : Gapext 0.5

Searched: 28348 seqs, 96089344 residues

Total number of hits satisfying chosen parameters: 28348

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 98

Maximum Match 100%

Listing first 45 summaries

Database :

1: p111:*

2: p112:*

3: p113:*

4: p114:*

Pred. No. is the number of results predicted by chosen 1 base
score greater than or equal to the score of the result in the pattern
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	38	73.1	2	hypothetical protein
2	35	67.2	2	hypothetical protein
3	35	67.3	2	hypothetical protein
4	35	67.3	2	hypothetical protein
5	35	67.3	2	hypothetical protein
6	35	67.3	2	hypothetical protein
7	35	67.3	2	hypothetical protein
8	35	67.3	2	hypothetical protein
9	35	67.3	2	hypothetical protein
10	34	65.4	2	hypothetical protein
11	34	65.4	2	hypothetical protein
12	34	65.4	2	hypothetical protein
13	33	63.5	2	hypothetical protein
14	33	63.5	2	hypothetical protein
15	33	63.5	2	hypothetical protein
16	33	63.5	2	hypothetical protein
17	33	63.5	2	hypothetical protein
18	33	63.5	2	hypothetical protein
19	33	63.5	2	hypothetical protein
20	33	63.5	2	hypothetical protein
21	33	63.5	2	hypothetical protein
22	32	61.5	2	hypothetical protein
23	32	61.5	2	hypothetical protein
24	32	61.5	2	hypothetical protein
25	32	61.5	2	hypothetical protein
26	32	61.5	2	hypothetical protein
27	32	61.5	2	hypothetical protein
28	32	61.5	2	hypothetical protein
29	32	61.5	2	hypothetical protein

30	32	61.5	344	2	A72716	probable hemolysin
31	32	61.5	348	2	A69922	hypothetical protein
32	32	61.5	358	2	G72584	putative hemolysin
33	32	61.5	362	2	119166	hypothetical protein
34	32	61.5	367	2	A66113	hypothetical protein
35	32	61.5	417	2	129198	hypothetical protein
36	32	61.5	425	2	B66892	VI polysaccharide
37	32	61.5	425	2	AH1041	VI polysaccharide
38	32	61.5	427	2	144520	VI polysaccharide
39	32	61.5	437	2	144509	VI polysaccharide
40	32	61.5	467	2	D84055	polysaccharide
41	32	61.5	501	2	F71965	polysaccharide
42	32	61.5	501	2	144542	polysaccharide
43	32	61.5	616	2	B67654	VI polysaccharide
44	32	61.5	684	2	F37694	VI polysaccharide
45	32	61.5	927	2	119110	VI polysaccharide

ALIGNMENTS

RESULT 1

F70082

hypothetical protein yxh

Database: Bacillus subtilis

Query: 05-Dec-1997 #sequence_revision 05-Dec-1997 #match_change 15 Feb-1999

Accession: F70082

RefSeq: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

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Accession: F70082

Job 215 EMBLSEARCH.224

RESULT 15

AE16.0

Hypothetical protein homolog (Uni422) (Imported) - list of amino acids (strain of H11262)

Species: *Escherichia coli*

Date: 27-Nov-2001 Accession: F01116.0

Accession: AE16.0

Glaser, P.; Frangoul, L.; Hughes, G.; Amend, A.; Kapur, P.; Berche, P.; Blocker, B.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

Authors: Karst, U.; Frangoul, L.; Hughes, G.; Amend, A.; Kapur, P.; Berche, P.; Blocker, B.; Jones, L.M.; Karst, U.

ok, G.; Schlegel, J.; Stoeck, N.; Berche, A.; Van Lee, B.; Voss, R.; Wobler, A.

Article: Comparative genomics of *Escherichia coli* strains

Reference number: AB1077; MIM:2157279; PMID:1177669

Accession: AE16.0

Status: Preliminary

Molecule type: DNA

Residues: 1-308 cDNA

Cross-reference: GI:1592022; EMBL:AC9653.1; F01116.0; GenBank:U00178

Experimental source: strain of H11262

Comments:

Access: Uni422

Similarity: conserved hypothetical protein y111

Query Match 63.5% Score 33.18 Z: length 308

Post-local similarity 54.5% Prod. No. 502

Matches 62 Conservative 23 Mismatches 37 Indels 02 Gaps 02

QY 1 MELPLAGKVL 11

11111 11

DA 48 LELFLANNRIL 58

Search completed: July 15, 2002, 14:23:21
Job time: 374 sec

CanCore version 4.5
Copyright (c) 1993 - 2000 Compucon Ltd

COM protein - protein search, using sw model

Run on: July 15, 2002, 17:59:17, Seed: 614001612, Max count:

Title: US-09-719-054A-4

SEQUENCE: 1 MELFLA3KRV1, 11

1 MEL.FI.A3KRV1, 11

See in table: H105JM62

Gapor 1(1.0) , Gapext. 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 106,274

Minimum IR seq length: 0

Maximum log seq length: 2000000000

[illegible][illegible]Listed in ISI 4⁵ Summary Index[illegible]

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analyzing the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	IR	IR
1	35	62.3	32.3	3	100
2	35	59.4	32.3	3	100
3	34	67.3	31.3	3	100
4	34	63.5	42.3	3	100
5	32	61.5	20.3	1	100
6	32	61.5	30.3	1	100
7	32	61.5	34.8	1	100
8	32	61.5	41.7	3	100
9	32	61.5	42.5	3	100
10	32	61.5	50.1	3	100
11	32	61.5	50.1	3	100
12	31	59.6	10.9	1	100
13	31	59.6	10.9	1	100
14	31	59.6	19.0	1	100
15	31	59.6	25.2	1	100
16	31	59.6	26.1	1	100
17	31	59.6	29.1	1	100
18	31	59.6	32.3	3	100
19	31	59.6	41.5	3	100
20	31	59.6	43.2	3	100
21	31	59.6	50.1	3	100
22	31	59.6	50.2	3	100
23	31	59.6	51.7	3	100
24	31	59.6	51.7	3	100
25	31	59.6	52.4	3	100
26	31	59.6	52.4	3	100
27	31	59.6	52.4	3	100
28	31	59.6	52.4	3	100
29	31	59.6	52.4	3	100
30	31	59.6	72.2	3	100
31	31	59.6	140.9	3	100
32	30.5	58.7	29.1	1	100
33	30	57.7	18.7	1	100

44	30	57.7	235	HMS_PESSE	1-43362	hamophilus
45	30	57.7	238	MSA_EARIN	05710	hamophilus
46	30	57.7	261	FAB1_EARIN	B44442	hamophilus
47	30	57.7	261	V602_RELTA	Q76010	hamophilus
48	30	57.7	407	EPA_NEMIA	Q91742	metamorph
49	30	57.7	307	ERA_NEMIA	Q76057	metamorph
40	30	57.7	343	CPFA_STRMO	Q73459	metamorph
41	30	57.7	375	WCC1_EGCHI	Q25205	metamorph
42	30	57.7	400	ACG9_EGCHI	P22651	metamorph
43	30	57.7	480	CAIA_EGCHI	P11571	metamorph
44	30	57.7	496	PLSH_C02ME	P10345	metamorph
45	30	57.7	398	AC1U_LONJME	P45850	metamorph

ALTIMETRY

```

1 RESUME: 1
2 LUKE_STAU LUKE_STAU STANDARD: PRI: 321 AA.
3 ID P41715;
4 DT 01-JUL-1993 (rel. 26, created)
5 DT 16-OCT-2001 (rel. 40, last sequence update)
6 DT 16-OCT-2001 (rel. 40, last annotation update)
7 DE Idoxycycline F subunit, precursor (gamma-hemolysin, gamma-1 subunit).
8 LN LUKE.
9 FT "Apoptosis during
10 infection: Firmicutes, Bacillus/Clostridium group;
11 Bacillus/Staphylococcus group; Staphylococcus.
12 Uni_Taxid 12607.
13 RN 111
14 SEQUENCE FROM N.A. AND SEQUENCE OF 26 66.
15 AC STRAIN MESA NO. 4;
16 EX METALINE 9224395; EMBL 157538;
17 RA Palmeri, A.; Nally, B.; Taki, K.; Kato, T.; Kanto, Y.;
18 "Molecular cloning and nucleotide sequence of a novel F component
19 gene (luke) from methicillin resistant Staphylococcus aureus."
20 J. Biochem. Biophys. Res. Commun. 184:640-646 (1992).
21 LN 121
22 SEQUENCE OF 27 85 AND 322-325.
23 AC STRAIN RMD 310926;
24 EX METALINE 9224395; EMBL 3467905;
25 RA "Muller, Y.; Palmeri, A.; Taki, H.; Kato, T.; Taki, Y.;
26 "The two Staphylococcus aureus F component factors, Idoxycycline and gamma-
27 hemolysin, share one component in common."
28 FBS Lett. 321:115-18 (1993).
29 C2 1 FUNCTION: Idoxycycline causes CYTOTOXIC CHANNEL IN POLYMERIZING/ACTIN
30 FIBRILS. GAMMA-HEMOLYSIN CAUSES HEMOLYSIS IN RED BLOOD CELLS.
31 SUPPORT: Idoxycycline consists of two protein components: F AND S;
32 GAMMA-HEMOLYSIN CONSISTS OF TWO PROTEIN COMPONENTS (H GAMMA-1 F
33 AND H-GAMMA-11).
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00 online compilation of the program (25, 1994) or
01 send an email to: license@cs.b.c.b.
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Quality Match	65.4%	Score 347	108	1	Fourth 611
Post-Love Similarity	77.8%	Freq. No. 245			
Matches	7	Conservation	1	104.1%	7
27	2	Enrichment	1		
16	479	Enrichment	487		

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1  RESULT      4
2  CAPL_STAND
3  1P  CAPL_STAND      STANDAPT:      PRG:      4.1 AA.
4  1P  1986:
5  01-FEB-1995 (Ref. 31, Updated)
6  01-FEB-1995 (Ref. 31, Last sequence update)
7  01-NOV-1995 (Ref. 32, Last annotation update)
8  CAPL protein.
9  CAPL.
10 Staphylococcus aureus.
11 Bacteria; Firmicutes; Bacilli; Clostridium group.
12 Bacillus subtilis group.
13 P81243.D (2005)
14 11
15 1P  SEQUENCE FROM N.A.
16 1P  STRAIN M.
17 1P  MONTIPUT GENES 370, 307, 304, 303, 302, 301, 300, 299, 298, 297, 296, 295, 294, 293, 292, 291, 290, 289, 288, 287, 286, 285, 284, 283, 282, 281, 280, 279, 278, 277, 276, 275, 274, 273, 272, 271, 270, 269, 268, 267, 266, 265, 264, 263, 262, 261, 260, 259, 258, 257, 256, 255, 254, 253, 252, 251, 250, 249, 248, 247, 246, 245, 244, 243, 242, 241, 240, 239, 238, 237, 236, 235, 234, 233, 232, 231, 230, 229, 228, 227, 226, 225, 224, 223, 222, 221, 220, 219, 218, 217, 216, 215, 214, 213, 212, 211, 210, 209, 208, 207, 206, 205, 204, 203, 202, 201, 200, 199, 198, 197, 196, 195, 194, 193, 192, 191, 190, 189, 188, 187, 186, 185, 184, 183, 182, 181, 180, 179, 178, 177, 176, 175, 174, 173, 172, 171, 170, 169, 168, 167, 166, 165, 164, 163, 162, 161, 160, 159, 158, 157, 156, 155, 154, 153, 152, 151, 150, 149, 148, 147, 146, 145, 144, 143, 142, 141, 140, 139, 138, 137, 136, 135, 134, 133, 132, 131, 130, 129, 128, 127, 126, 125, 124, 123, 122, 121, 120, 119, 118, 117, 116, 115, 114, 113, 112, 111, 110, 109, 108, 107, 106, 105, 104, 103, 102, 101, 100, 99, 98, 97, 96, 95, 94, 93, 92, 91, 90, 89, 88, 87, 86, 85, 84, 83, 82, 81, 80, 79, 78, 77, 76, 75, 74, 73, 72, 71, 70, 69, 68, 67, 66, 65, 64, 63, 62, 61, 60, 59, 58, 57, 56, 55, 54, 53, 52, 51, 50, 49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1.
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10	069668Z				
11	15-DIST-1998 (Rel. 37, created)				
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13	15-DIST-2001 (Rel. 40, last amended run update)				
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[illegible]

R9 SEQUENCE FROM N.A.
 R0 121
 R1 STRAIN-CHEC 1551 / oshkosh
 R2 Fleischmann R., Alirol D., Eisen J.A., Carpenter L., White O.,
 R3 Peterson J., Leroy P., Ivansson R., Gattin M., Hall P., Hickey E.,
 R4 Kraljic J., Reischman W., Derynck L.A., De Groot M., Albrecht S.L.,
 R5 Decker A., Oberbach T., Wolfman J., Shmidt H., Gill J., Mironov A.,
 R6 Bushal W.
 R7 "Whole genome comparison of Mycobacterium tuberculosis clinical and
 R8 laboratory strains."
 R9 10.1093/nar/gkn147
 R0 11 FURTHER MAY HAVE A ROLE IN DNA REPAIR. IT SEEMS TO BE INVOLVED
 R1 IN DNA REPAIR, INHERENT REPAIR, NATURAL REPAIR, AND REPAIR. IT
 R2 MAY ACT WITH REPAIR AND REPAIR (BY DIRECTLY).
 R3 11 SIMILARITY: BELONGS TO THE REPAIR FAMILY.
 R4 12

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EMBL: A00021761; EMBL047.1; 1
EMBL: A00071761; A004187.1; 1
EMBL: M10118; 1
D06: InterPro: IP001567; 1
D06: InterPro: IP001567; HM 1
D06: InterPro: IP0000943; R06R; 1
D06: InterPro: IP0029861; Toprim; 1
D06: Pfam: PF02142; R06R; 1
D06: Pfam: PF01751; Toprim; 1
EMBL: X000278; HM1; 1
EMBL: S0004943; Toprim; 1
D06: PROSITE: PS01400; R06R; 1
EMBL: repeat: EMBL recombinant; Zinc finger; complete protein; 1
EMBL: repeat: 56; 71
EMBL: repeat: 204 AA; 22177 MW; 50812956.47777777; GR564;

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100


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00      Lysyl tRNA(Lys).
01  - SUBUNIT: HOMODIMER (BY SIMILARITY).
02  - SUBCELLULAR LOCATION: Cytoplasmic.
03  - SIMILARITY: BELONGS TO CLASS II AMIN-ACYL TRNG. PROTEINASE FAMILY.
04  -----
05  This SWISS-Prot entry is copyright. It is produced through a collaboration
06  between The Swiss Institute of Bioinformatics and The EMBL outstation
07  The European Bioinformatics Institute. There are no restrictions on its
08  use by non-profit institutions as long as its content is in no way
09  modified and this statement is not removed, misrep. by, and for commercial
10  entities requires a license agreement (see http://www.ebi.ac.uk/submit/
11  or send an email to license@ebi.ac.uk).
12  -----
13  EMBL: AB001456; A00059.1.1.
14  BSSP: P14W25; 11YL.
15  InterPro: IP0002409; AA:trna_lyse_2.
16  InterPro: IP0002409; trna-synt_2.
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18  Pfam: PF00152; trna_synth_2.1.
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21  PRSITE: PR00042; TRNACYSYNTS.
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48  PRSITE: PR00042; AA:trna_lyse_2.1.
49  PRSITE: PR00042; AA:trna_lyse_2.1.
50  PRSITE: PR00042; AA:trna_lyse_2.1.
51  PRSITE: PR00042; AA:trna_lyse_2.1.
52  PRSITE: PR00042; AA:trna_lyse_2.1.
53  PRSITE: PR00042; AA:trna_lyse_2.1.
54  PRSITE: PR00042; AA:trna_lyse_2.1.
55  PRSITE: PR00042; AA:trna_lyse_2.1.
56  PRSITE: PR00042; AA:trna_lyse_2.1.
57  PRSITE: PR00042; AA:trna_lyse_2.1.
58  PRSITE: PR00042; AA:trna_lyse_2.1.
59  PRSITE: PR00042; AA:trna_lyse_2.1.
60  PRSITE: PR00042; AA:trna_lyse_2.1.
61  PRSITE: PR00042; AA:trna_lyse_2.1.
62  PRSITE: PR00042; AA:trna_lyse_2.1.
63  PRSITE: PR00042; AA:trna_lyse_2.1.
64  PRSITE: PR00042; AA:trna_lyse_2.1.
65  PRSITE: PR00042; AA:trna_lyse_2.1.
66  PRSITE: PR00042; AA:trna_lyse_2.1.
67  PRSITE: PR00042; AA:trna_lyse_2.1.
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69  PRSITE: PR00042; AA:trna_lyse_2.1.
70  PRSITE: PR00042; AA:trna_lyse_2.1.
71  PRSITE: PR00042; AA:trna_lyse_2.1.
72  PRSITE: PR00042; AA:trna_lyse_2.1.
73  PRSITE: PR00042; AA:trna_lyse_2.1.
74  PRSITE: PR00042; AA:trna_lyse_2.1.
75  PRSITE: PR00042; AA:trna_lyse_2.1.
76  PRSITE: PR00042; AA:trna_lyse_2.1.
77  PRSITE: PR00042; AA:trna_lyse_2.1.
78  PRSITE: PR00042; AA:trna_lyse_2.1.
79  PRSITE: PR00042; AA:trna_lyse_2.1.
80  PRSITE: PR00042; AA:trna_lyse_2.1.
81  PRSITE: PR00042; AA:trna_lyse_2.1.
82  PRSITE: PR00042; AA:trna_lyse_2.1.
83  PRSITE: PR00042; AA:trna_lyse_2.1.
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98  PRSITE: PR00042; AA:trna_lyse_2.1.
99  PRSITE: PR00042; AA:trna_lyse_2.1.
100 PRSITE: PR00042; AA:trna_lyse_2.1.

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00  between The Swiss Institute of Bioinformatics and The EMBL outstation
01  The European Bioinformatics Institute. There are no restrictions on its
02  use by non-profit institutions as long as its content is in no way
03  modified and this statement is not removed, misrep. by, and for commercial
04  entities requires a license agreement (see http://www.ebi.ac.uk/submit/
05  or send an email to license@ebi.ac.uk).
06  -----
07  EMBL: AB000548; A00075.1.1.
08  BSSP: P14W25; 11YL.
09  InterPro: IP0002409; trna-synt_2.
10  InterPro: IP0002409; trna-synt_lys_2.
11  InterPro: IP0002409; trna-synt_2.
12  InterPro: IP0002409; trna-synt_2.
13  InterPro: IP0002409; trna-synt_2.
14  InterPro: IP0002409; trna-synt_2.
15  InterPro: IP0002409; trna-synt_2.
16  InterPro: IP0002409; trna-synt_2.
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20  InterPro: IP0002409; trna-synt_2.
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24  InterPro: IP0002409; trna-synt_2.
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27  InterPro: IP0002409; trna-synt_2.
28  InterPro: IP0002409; trna-synt_2.
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30  InterPro: IP0002409; trna-synt_2.
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32  InterPro: IP0002409; trna-synt_2.
33  InterPro: IP0002409; trna-synt_2.
34  InterPro: IP0002409; trna-synt_2.
35  InterPro: IP0002409; trna-synt_2.
36  InterPro: IP0002409; trna-synt_2.
37  InterPro: IP0002409; trna-synt_2.
38  InterPro: IP0002409; trna-synt_2.
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40  InterPro: IP0002409; trna-synt_2.
41  InterPro: IP0002409; trna-synt_2.
42  InterPro: IP0002409; trna-synt_2.
43  InterPro: IP0002409; trna-synt_2.
44  InterPro: IP0002409; trna-synt_2.
45  InterPro: IP0002409; trna-synt_2.
46  InterPro: IP0002409; trna-synt_2.
47  InterPro: IP0002409; trna-synt_2.
48  InterPro: IP0002409; trna-synt_2.
49  InterPro: IP0002409; trna-synt_2.
50  InterPro: IP0002409; trna-synt_2.
51  InterPro: IP0002409; trna-synt_2.
52  InterPro: IP0002409; trna-synt_2.
53  InterPro: IP0002409; trna-synt_2.
54  InterPro: IP0002409; trna-synt_2.
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56  InterPro: IP0002409; trna-synt_2.
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58  InterPro: IP0002409; trna-synt_2.
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60  InterPro: IP0002409; trna-synt_2.
61  InterPro: IP0002409; trna-synt_2.
62  InterPro: IP0002409; trna-synt_2.
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67  InterPro: IP0002409; trna-synt_2.
68  InterPro: IP0002409; trna-synt_2.
69  InterPro: IP0002409; trna-synt_2.
70  InterPro: IP0002409; trna-synt_2.
71  InterPro: IP0002409; trna-synt_2.
72  InterPro: IP0002409; trna-synt_2.
73  InterPro: IP0002409; trna-synt_2.
74  InterPro: IP0002409; trna-synt_2.
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79  InterPro: IP0002409; trna-synt_2.
80  InterPro: IP0002409; trna-synt_2.
81  InterPro: IP0002409; trna-synt_2.
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84  InterPro: IP0002409; trna-synt_2.
85  InterPro: IP0002409; trna-synt_2.
86  InterPro: IP0002409; trna-synt_2.
87  InterPro: IP0002409; trna-synt_2.
88  InterPro: IP0002409; trna-synt_2.
89  InterPro: IP0002409; trna-synt_2.
90  InterPro: IP0002409; trna-synt_2.
91  InterPro: IP0002409; trna-synt_2.
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93  InterPro: IP0002409; trna-synt_2.
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97  InterPro: IP0002409; trna-synt_2.
98  InterPro: IP0002409; trna-synt_2.
99  InterPro: IP0002409; trna-synt_2.
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LR IntAct: IPRO00554; Ribosomal_S7E.
 DR Pfam: PF01251; Ribosomal_S7E; 1.
 DR ProDom: PD006274; Ribosomal_S7E; 1.
 DR PROSITE: PS00944; RIBOSOMAL_S7E; PALSE_NRM.
 KW Ribosomal protein Acetylation; Multisubunit family.
 FT INIT_MET 0 0
 FT MOTIF 1 1 ACETYLATION.
 FT COMPLET 2 2 F / D (R R E 2).
 SL SEQUENCE 189 AA; 2142; MW: 25660.270; CASRES: C9011

Query Match 59.6%; Score 31; DB 1; Length 189
 Best Local Similarity 66.7%; Prod. No. 49
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0

4 LEAFBLVYL 1
 50 LEAFBLVYL 99

RESULT 14

V574_MEL1A STANDARD; FRT; 159 AA.

01-NOV-1997 (Rel. 35, Created)
 01-NOV-1997 (Rel. 35, Last sequence update)
 16-07-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MJ0573.
 GN MJ0573.
 OS Methanococcus jannaschii.
 LC Archaeal hyperthermophilic anaerobic coccus.
 OX Methanococcus.
 OX NCBI_TaxID:2190;
 RN 11

SEQUENCE FROM N.A.
 RC STRAIN JAL-1 / DSM 5261 / ATCC 43047;
 RX MEDLINE:96337999; PubMed:8648087;

RA But C.J., White G., Olsen G.J., Zhou L., Fleischmann R.,
 RA Sutton G., White J.A., Fierman J.D., Clayton J.A., Anderson J.L.,
 RA Kozlowski A.P., DeLong E.P., Tomb J.F., Adams M.D., Belknap J.L.,
 RA Goodbye K., Venter A., Weisbach F.S., Weiss R., Holt R.A.,
 RA Scott J.L., Goodenough J.M., Woelfel J.P., Fritchman J.B., Mungai P.,
 RA Hootnick T., Kelley J.M., Peterson J.L., Faller P.A., Hunt J.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kallio R.P., Kozlosky M.,
 RA Klenk H.P., Fraser M., Smith H., Woese C.R., Woelfel J.P.,
 RA "Complete genome sequence of the methanophilic archaeon, Methanocaldococcus jannaschii".
 RL Science 273:1056-1073(1996).

1-1 SIMILARITY: PERONS TO THE DSM/ATCC FAMILY.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC use by non-profit institutions as long as its content is in no way
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DR EMBL: 067506; AAB0573.1; -
 DR IIR: M10573; -
 KW Hypothetical protein; Complete Proteome.
 SL SEQUENCE 189 AA; 21198 MW; 47173994AMBER; C9011

Query Match 59.6%; Score 31; DB 1; Length 189
 Best Local Similarity 66.7%; Prod. No. 49
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0

05 1 MEL1AG 7
 111111
 98 MEL1AG 104

RESULT 14

K57R_YEAST STANDARD; FRT; 190 AA.

01-FEB-1996 (Rel. 33, Created)
 01-FEB-1996 (Rel. 33, Last sequence update)
 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 40S ribosomal protein S7B.
 GN R057B OR YH0296C (8 R212).

OS Saccharomyces cerevisiae (Baker's yeast).

LC Eukaryotic, Fungal, Ascomycota, Saccharomycetes, Saccharomycetaceae, Saccharomyces.

OX Saccharomyces cerevisiae, Saccharomycetaceae, Saccharomycetes.
 OX NCBI_TaxID 4932;
 RN 11

SEQUENCE FROM N.A.

RC STRAIN S288C / FY1679;
 RX MEDLINE:96467601; PubMed:8771715;
 RA Garcia-Randazzo J.M., Moskvina J., Talvez A.;

RA "Sequence analysis of a 14.2 kb fragment of Saccharomyces cerevisiae
 RA chromosome XIV that includes the YH15, ERN14 and gal 82 genes and
 RA four new open reading frames.";
 RL Yeast 12:599-608(1996).

1-1 SIMILARITY: PERONS TO THE S7E FAMILY OF RIBOSOMAL PROTEINS.

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CC or send an email to license@ebi.ac.uk).

DR EMBL: X85811; CA59482.1; -

DR EMBL: 271472; CA59572.1; -

16 EMBL: 5905340; R057B.
 DR InterPro: IPRO00554; Ribosomal_S7E.

DR Pfam: PF01251; Ribosomal_S7E; 1.
 DR ProDom: PD006274; Ribosomal_S7E; 1.
 DR PROSITE: PS00948; RIBOSOMAL_S7E; 1.

14 RIBOSOMAL PROTEIN; Multisubunit family.
 SL SEQUENCE 190 AA; 21634 MW; 466538745FAFAH C9064;

Query Match 59.6%; Score 31; DB 1; Length 190
 Best Local Similarity 66.7%; Prod. No. 31
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0

05 3 LEAFBLVYL 11
 11111111

06 91 LEAFBLVYL 99

RESULT 15

V296_TRVSY STANDARD; FRT; 272 AA.

01-V296-TRV S STANDARD; FRT; 272 AA.
 DR P05073;
 DR 13-AUG-1987 (Rel. 05, Created)
 DR 13-AUG-1987 (Rel. 05, Last sequence update)
 DR 15-DEC-1998 (Rel. 37, Last annotation update)

DE 29 kDa protein.
 OS Tobacco etiolate virus (strain 579) and

OS Tobacco etiolate virus (strain 580);

OS Virus; RNA virus; external ribonucleic acid (RNA) virus.

OX NCBI_TaxID 12298; 12297;
 RN 11

SEQUENCE FROM N.A.

RC STRAIN 579;
 RX EMBL: 9904943; PubMed: 666907;

RA Hamilton W.D.O., Roberts M., Robinson D.J., Raulicomb D.C.;
 RA "The complete nucleotide sequence of tobacco etiolate virus RNA-1.";
 RL J. Gen. Virol. 68:2561-2575(1987).

121

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84 SEQUENCE FROM N.A.
85 STRAIN SYM:
86 Baccara M., Hamilton W., G. Baulcombe D.C.
87 "The organisation and inter-viral homologies of genes at the 3' end of
88 tobacco etch virus RNA."
89 EMBO J. 5:223-231 (1986).
90
91
92
93 SEQUENCE FROM N.A.
94 STRAIN ESQ:
95 MEDLINE 86176720; PubMed 3960718;
96 Corbettsson B.J.C., Lamborn B.J.M., Hendryde P.L., Red J.P.
97 "Analysis of the genome structure of tobacco etch virus strain
98 ESQ."
99 Nucleic Acids Res. 14:2157-2169 (1986).
100
101 MISCELLANEOUS: THIS PROTEIN IS BEING TO GO FOR THE INTRAVENOUS
102 INVOLVED IN VIRAL CELL CELL TRANSFERT.
103
104
105 This SWISS-PROT entry is copyright. It is produced through a collaboration
106 between the Swiss Institute of Bioinformatics and the EMBL outstation.
107 The European Bioinformatics Institute. There are no restrictions on its
108 use by non-profit institutions as long as its content is in no way
109 modified and this statement is not removed. Usage by and for commercial
110 entities requires a license agreement (See http://www.ebi.ac.uk/seqdb/
111 or send an email to license@ebi.ac.uk)
112
113
114 EMBL: X00085; CAA27420.1;
115 EMBL: X06172; CAA29538.1;
116 EMBL: D00195; BAA0112.1;
117 F1R: A01144; W00V2P;
118 F1R: S02404; S02409;
119
120 SEQUENCE: 252 AA; 28846 MW; 5A7469606519AA; 38944;

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Query Match: 59.6%; Score 41; Dir 1; Length 252;
Best Local Similarity: 66.7%; Prod. No. 41;
Matches: 62; Conserved: 2; Mismatches: 1; Indels: 0; Gaps:
QY 1 MELFLAGRR 9
+|||: |||
DH 25 TELPVAGRR 33

```

Search completed: July 15, 2002, 14:05:04
Job time: 447 sec

XX Claim 2: Fig 6: 1ppp: English.

XX This sequence represents a human accessory sperm protein (P4).

XX P4 is a human homologue of the hamster P2b accessory sperm protein

XX which is acquired during epididymal transit. P2b is known to play

XX a role in sperm interaction as demonstrated by the ability of

XX anti-P2b antibodies to inhibit sperm/zona pellucida binding in

XX vitro and in vivo. It exhibits immunoreactivity for P2b and is

XX used to actively immunize male hamsters. Similarly, P4 has potential

XX for use in an immunovaccine against varicella in humans. P4

XX is specifically expressed in the epididymis, which suggests its

XX potential as an immunovaccine target. An immunovaccine

XX vaccine may comprise at least fragments of P4 (AAV5/27-7; AAV5/29-5),

XX and an immune response should be generated against the P4 fragments

XX when administered to men. As the blood-testis barrier is not present in

XX the epididymis, the antibodies should reach the spermatozoa and

XX neutralise the fertilising ability of the spermatozoa. Thus contraindicating

XX an immunovaccine for contraception.

XX Sequence: 209 AA:

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XX The invention relates to DNA encoding a human carbonyl reductase protein

XX (HCRD) sequence. Also claimed are: a probe that hybridizes to the DNA

XX sequence; an expression vector containing the DNA sequence; and a host

XX cell producing the vector. The enzyme catalyzes the reduction of

XX carbonyls to alcohols; physiologically functioning as dehydrogenase of

XX prostaglandin of hydroxysteroids, as well as in drug metabolism. The cell

XX can be used to produce a recombinant human carbonyl reductase protein

XX which can be used to treat inflammatory or immunological disorders.

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[illegible]

XX Homo sapiens.
 OS
 XX DE19820190-A1.
 XX
 XX 04-NOV-1999.
 XX
 XX 28-APR-1998; 58DE-1020190.
 XX
 XX 28-APR-1998; 58DE-1020190.
 XX
 XX (MHA-1) METACIN CES CHIMBESCHING MRA
 XX
 XX Rosemary A. Griebel T. Miesman R. Schell A. Ellender C. Ellis B.
 XX
 XX WPI: 1999-60196/74
 XX
 XX N (SDB): AA052945.
 XX
 XX New human testis/acid sequences from pancreatic tumors and normal
 XX
 XX proteins.
 XX
 XX claim 23; page 424; 502pp; German.
 XX
 XX This invention describes novel polypeptides and their associated proteins
 XX
 XX acids derived from human pancreatic tumor tissue which have suppressive
 XX
 XX activity. The sequences are also useful in producing pharmaceutical
 XX
 XX compositions for treatment of pancreatic tumors. AA052945-7417.
 XX
 XX represent protein fragments encoded by the human gene for tumor suppressor
 XX
 XX library derived expressed sequence tag (EST) sequences deposited in
 XX
 XX AA052958-25004.
 XX
 XX
 XX Sequence 443 AA:
 XX

Query Match 100.0%; Score 52; 0H 20; Length 133;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 MELFLACRVI 11

DB 90 mellacrv 100

RESULT 12

AA0529292

XX ID AA0529292 standard; peptide; 11 AA.

XX AC AA0529292

XX XX

XX 09-FEB-2000 (first entry)

XX XX

XX Human acrosomal sperm protein p34 antigenic peptide #1.

XX XX

XX p34; acrosomal sperm protein; p34; homologous immunoreactive protein;

XX XX

XX acrosome; epididymis; female; maturation; interaction; mature;

XX XX

XX spermatozoan zona pellucida; vaccine; antigen; immunization; no

XX XX

XX fertilisation; fragment; antigenic.

XX OS

XX Homo sapiens.

XX XX

XX 08598549 A.

XX XX

XX 23-NOV-1999.

XX XX

XX 08-NOV-1998; 38US-0090567.

XX XX

XX 08-NOV-1998; 38US-0090567

XX XX

XX (IMMUNO) IMMUNON INC.

XX XX

XX Sullivan R. Berube R. Gaudreault C. Isidore C.

XX XX

XX WPI: 2000-02701-702

XX Antigenic fragments to human acrosomal sperm protein p34 for
 XX
 XX immunoreception.
 XX
 XX claim 2; column 17; 19pp; English.
 XX
 XX This separate reference an antigenic fragment (#1) of human acrosomal
 XX
 XX sperm protein p34. p34 is a human homologue of the hamster p26.
 XX
 XX acrosomal sperm protein which is acquired during epididymal transit.
 XX
 XX p26 is known to play a role in female interaction as demonstrated by
 XX
 XX binding in vitro and in vivo. It exhibits immunoreactive properties
 XX
 XX when used to actively immunise male hamsters. Similarly, p34 has
 XX
 XX potential for use in an immunovaccine vaccine in hamster. p34
 XX
 XX is specifically expressed in the epididymis, which supports its
 XX
 XX potential as an immunoreactive vaccine. An immunovaccine vaccine
 XX
 XX vaccine may comprise antigenic fragments of p34 (vacc). This sequence of
 XX
 XX AA0529292 and an immune response should be generated against the p34
 XX
 XX fragments when administered to men. As the blood-testis barrier is not
 XX
 XX present in the epididymis, the antibodies should reach the spermatozoa
 XX
 XX and neutralise the fertilising ability of the spermatozoa, thus
 XX
 XX conferring an immunoreceptive protection.
 XX
 XX
 XX Sequence 11 AA:
 XX

Query Match 92.7%; Score 48; 0H 21; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0922;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 MELFLACRVI 10

DB 1 mellacrv 10

RESULT 13

AA030266

XX ID AA030266 standard; protein; 297 AA.

XX AC AA030266;

XX XX

XX 18-DEC-2001 (first entry)

XX XX

XX Novel human secreted protein #757.

XX XX

XX Human vaccination gene therapy; nutritional supplement;

XX XX

XX stem cell proliferation; hematopoiesis; active tissue regeneration;

XX XX

XX immune suppression; immune stimulation; and inflammation; leukaemia.

XX OS

XX Homo sapiens.

XX XX

XX W0200179449-A2.

XX XX

XX 25-EPT-2001.

XX XX

XX 16-APR-2001; 299US-0898556.

XX XX

XX 18-APR-2000; 280US-0552929.

XX XX

XX 26-JAN-2001; 2001US-0770160.

XX XX

XX (HYSE-) HYSEQ INC.

XX XX

XX Tang YT, Liu C. Immune RT;

XX XX

XX WPI: 2001-611725/70.

XX XX

XX Nucleic acids encoding a range of human polypeptides, useful in genetic

XX XX

XX vaccination, testing and therapy.

XX XX

XX claim 29; page 269-270; 765pp; English.

XX XX

XX The invention relates to novel human secreted polypeptides. The

XX XX

XX polypeptides are useful for

determining the presence of or predisposition to a disease associated
 with altered levels of polypeptide. The polypeptides are also useful for
 identifying agents (antagonists and antagonists) that bind to them, cells
 expressing the proteins are useful for identifying a therapeutic agent
 for use in treatment of a pathology related to aberrant expression of
 physiological interactions of the polypeptides. Vaccines comprising
 the nucleic acids encoding the polypeptides and cells that secrete
 engineered to express them are also useful for producing the proteins.
 The proteins are useful in genetic variation, testing and
 therapy, and can be used as nutrient supplements. They may be used to
 increase stem cell proliferation to regulate hematopoiesis and in
 bone, cartilage, tendon, and/or nerve tissue growth or repair after
 immune suppression and/or stimulation; as anti-inflammatory agents; and
 in treatment of leukemias. AA029510-AA044444 represent the amino acid
 sequences of novel human secreted proteins of the fibronectin
 XX
 XX
 S0 Sequence 297 AA:
 Query Match 96.4% Score 473.18 E27 Length 173
 Best Local Similarity 100.00% Ident. No. 0.17
 Matches 197 Conserved 197 Mismatches 0 Gaps 0
 QY 2 HELPLAGREV.11
 1111111111
 Db 7 c11a2rrv1.16
 RESULT 14
 AA07997
 ID AA067997 standard: Protein: 190 AA.
 XX
 AC AA067997:
 XX
 DE 27 FEB 2002 (first entry)
 XX
 DE Propionibacterium arvens immunogenic protein #28893.
 XX
 KW SAPHO syndrome; synovitis; arroy; pustulosis; hyperostosis; osteomyelitis;
 KW growth; endophthalmitis; bone; joint; ocular; nervous system; AIDS;
 KW inflammatory lesion; are vulvaritis; erythema; linked immunosyctoid assay
 KW dermatologically; osteopathy; neuropathic.
 XX
 OS Propionibacterium arvens.
 XX
 PN W0200181581-A2.
 XX
 PN 01-NOV-2001.
 XX
 PF 20-APR 2001: 2001W010512865.
 XX
 XX 21 APR 2000: 2000W010512865.
 XX 02 JUN 2000: 2000W010512865.
 XX 07 JUL 2000: 2000W010512865.
 XX
 PA (GPR1) (GPR1A) (GPR1A)
 XX
 XX Skeiky YAM, Persing RH, Mithum JL, Wang SS, Phatla A;
 XX L'etisonneuve J, Zhang Y, Jon S, Carter D;
 XX
 XX WP1: 2001 61674771.
 XX N F0303: AA057971.
 XX
 P1 Propionibacterium arvens polypeptides and nucleic acids useful for
 P1 vaccinating against and diagnosing infections, especially useful for
 P1 treating are vulvaritis.
 XX
 XX Example 1: SEQ ID No 29192: 100pp; English.
 XX
 XX Sequences AA049105-AA06047 represent Propionibacterium arvens immunogenic
 XX polypeptides. The proteins and their associated DNA sequences are used in
 XX the treatment, prevention and diagnosis of medical conditions caused by
 XX P. arvens. The disorders include SAPHO syndrome (synovitis, arroy,

pustulosis, hyperostosis and osteomyelitis), erythema and endophthalmitis;
 P. arvens is also involved in infections of teeth, joints and the central
 nervous system, however, in the pathogenicity involved in the inflammatory
 lesions associated with are vulvaritis. A method for detecting the
 presence or absence of P. arvens in a patient comprises conducting a
 sample with a binding agent that binds to the proteins of the invention
 and determining the amount of bound protein in the sample. The
 polypeptides may be used as antigens in the production of the
 specific for P. arvens proteins. These antibodies can be used to
 downregulate expression and activity of P. arvens polypeptides and
 therefore treat P. arvens infections. The antibodies may also be used as
 diagnostic agents for determining P. arvens presence, for example, by
 enzyme-linked immunosorbent assay (ELISA).
 XX
 XX Note: The sequence data for this patent did not form part of the prior art
 or specification, but was obtained in electronic format directly from WPI
 at <http://wpi.int/Pub/Publicated-pat-sequences>.
 XX
 XX
 S0 Sequence 140 AA:
 Query Match 79.8% Score 467.18 E27 Length 190
 Best Local Similarity 72.7% Ident. No. 187
 Matches 87 Conserved 197 Mismatches 3 Gaps 0
 QY 1 HELPLAGREV.11
 1111111111
 Db 150 ms111rrv1.160
 RESULT 15
 AA033206
 ID AA033206 standard: Protein: 244 AA.
 XX
 AC AA033206:
 XX
 DE 18-NOV-1999 (first entry)
 XX
 DE Mouse diuretic/protease protein.
 XX
 KW Diuretic/protease protein; kidney tissue; 4-oxo-alpha-ketone; alpha-ketone;
 KW aromatic; orthoquinone; treatment; gene therapy; diagnosis; disorder;
 KW diabetes; diabetic; kidney insufficiency; are related arethrosis;
 KW drug screening; mutagen.
 XX
 XX
 OS Mus sp.
 XX
 PN W09946409-A1.
 XX
 PN 16-SEP-1999.
 XX
 PF 11 MAR 1999: 99W01001194.
 XX
 XX 12 MAR 1998: 98P00000195.
 XX 03 DEC 1998: 98P00000195.
 XX
 XX (TAIS) (TAIS) (TAIS) (TAIS)
 XX
 PA Nakagawa J, Yoshimoto M;
 XX
 XX WP1: 1999 551402746.
 XX N F0303: AA033206.
 XX
 P1 Diuretic/protease protein localized in kidney tissue used for treatment and
 P1 diagnosis of, are diabetes.
 XX
 XX Claim 3: Page 55 56: 62pp; Japanese.
 XX
 XX This invention describes novel diuretic/protease (or) protein
 XX isolated from mouse and human and which are expressed specifically
 XX in kidney tissue. The proteins of the invention have high proteolytic
 XX activity on 4-oxo-alpha-ketone and aromatic orthoquinones
 XX as substrates. The liver protein and its encoding nucleic acid can be
 XX used for the treatment (including gene therapy) and diagnosis of diseases

CC With which the protein is associated, including complications of
 CC diabetes, diabetic kidney insufficiency, and age-related
 CC arteriosclerosis; also screening of potential drugs for treatment of
 CC these disorders. This sequence represents the murine dicarboxylate
 CC protein described in the invention.
 XX

Sequence 244 AA

Query Match 59.2%; Score 36; DE 29; Length 214;
 Best Local Similarity 72.7%; Pred. No. 23;
 Matches 8, Conservative 1, Mismatches 2, Indels 0, Gaps 0;

QY 1 MELFLAGRRVL 11
 1:1 |||||
 Db 1 mdglagrral 11

Search completed: July 15, 2002, 13:58:46
 Job time: 359 sec

GenBank version 4.5
Copyright (c) 1993 - 2000 CompuLink Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 14:03:21 ; Start time 27.02 seconds
(without software)

1999. *Millie's* *U.S. Fish & Wildlife*

Title: US-19-716-053A-9

SEQUENCE: 19KARCSJPH: 11

Scoring table: BLOSSUM62

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Maximum Likelihood Estimation

Post-processing. Min min May 09

Listing first 45 summaries

Database : PIR_71 : ★

2000

[illegible]

pred. No. is the number of results pr

and is derived by analysts of the lot

SUMMARY

References

[illegible]

1	40	66.7	83	2	MI0974
2	40	66.7	83	2	MI0974

SUMMARY

Result No.	Score	Query Match	Length	DB	ID
1	46	54.7	82	2	AB0399
2	40	66.7	83	2	AB0374
3	39	55.1	470	2	S2124
4	36	60.3	104	1	U41578
5	36	50.3	104	2	A01276
6	36	50.3	104	2	AF6117
7	36	50.3	104	2	AF11952
8	36	50.3	132	2	A05022
9	36	50.3	132	2	E97893
10	36	50.3	511	2	S78104
11	36	50.3	946	2	E96568
12	36	50.3	5476	3	S47823
13	35	58.3	83	2	H01190
14	35	58.3	83	2	A56372
15	35	58.3	418	2	S99706
16	35	58.3	420	2	BB0164
17	35	58.3	483	2	AF1898
18	35	59.3	723	2	E62910
19	35	59.3	729	2	E44967
20	35	58.3	832	2	A11246
21	35	58.3	833	2	SI9087
22	35	58.3	844	2	S3865
23	35	58.3	867	1	GMMS1A
24	35	58.3	880	2	S00670
25	35	58.3	886	2	A2442
26	35	58.3	2339	2	A15792
27	34	56.7	99	2	A05199
28	34	56.7	170	2	E70608
29	34	56.7	309	2	E43752

RESULTS

hypothetical protein	40	56.7	474	2	852618
hypothetical protein	41	56.7	474	2	AP242
17 protein - varo	34	56.7	443	1	WVZV17
17L protein - varo	32	56.7	443	2	642511
K17 protein - vari	44	56.7	443	2	436843
hypothetical protein	44	56.7	443	2	626493
17L protein - vari	35	56.7	443	2	672158
hypoxanthase 11 -	37	56.7	433	2	777444
probable membrane	34	56.7	437	2	557073
protein P0011.8 [1]	48	56.7	733	1	086258
retrovirus-related	40	56.7	814	1	GNSNP1
14.6 kDa sulfoxide	34	56.7	815	2	664949
14.6 kDa sulfoxide	41	56.7	815	2	P90951
14.6 kDa sulfoxide	42	56.7	815	2	882137
14.6 kDa sulfoxide	43	56.7	815	2	BB5800
hypothetical protein	34	56.7	1257	2	791020

RESULT 1
AB0009
GenBankLink: [http://www.ncbi.nlm.nih.gov/BLAST/?term=AB0009] Versinia pestis (strain C-72)
Species: Versinia pestis
Created: 02 Nov 2001 #seqrevs_revised: 02 Nov 2001 #cvt_copies: 02-Nov-2001
Accession: AB0009
Etkanhill, J.; Wren, B.W.; Thomson, N.P.; Tibball, R.W.; Holden, M.T.; De
Groot-Fairman, A.M.; Chilworth, T.; Cronin, A.I.; Davies, R.M.; Davis, P.; Do
Nig, M.J.; Kirby, K.J.; Simmonds, M.J.; Shelton, J.; Stevens, K.; Whithead, S.
Nucleic Acids Res 29(2): 427-427, 2001
Allies genome sequence of *Versinia pestis*, the causative agent of plague.
Accession number: AB0001; MIMD21470418; PMID:11566560
A.Accession: AB0009
A.Status: Preliminary
A.Molecule Type: DNA
A.Restriction: 1, 62 - Kbp
A.Coverage: 100%
A.Length: 188K
A.Sequence:

Genotype Match: 66.78% Score: 439 DB:2 Length: 623
Host: Local Similarity: 66.78% Fred: No, 1-4
Matches: 6, Mismatch: 2, Mismatches: 1, Indels: 0, Gaps: 0
ID: 15 CHAKALIN 24
CY: 1 CHAKALIN 9
III: III
ID: 15 CHAKALIN 24
RESULT: 2
AH0974
Salmonella enterica subsp. enterica serovar Typhimurium (strain
O:3,12:H:15) isolated from a human, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649

[illegible]

	Score	Logit
Query Mat' 1	60.0%	1.4
Best Local Similarity	54.5%	
Matches	47	Matches
	47	Matches
1. CHARACTER	11	
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	1111	
80 CHARACTER	99	

RESOL. 7
AM1052

Species: *Salmonella enterica* subsp. *enterica* serovar Typhimurium
 A Note: This species has also been called *Salmonella typhimurium*
 Date: 09-Nov-2001
 Accession: AF1072
 Accession: AF1072

Received 12 November 2001; accepted 12 December 2001
 Correspondence: Dr. J. M. S. Simões, Laboratório de Genética, Instituto de Física de Caruaru, Universidade Federal de Pernambuco, Av. Prof. Moraes Cabral, 1212, 55072-910, Caruaru, PE, Brazil.
 E-mail: jmsimoes@fisica.ufpe.br
 © 2002 Blackwell Science Ltd, *Journal of Internal Medicine* 252: 361–367

A Accession: A0102
 A Medium: Fertilizer
 A Molecular type: DNA
 A Bioscience: 1104-1105
 A Cross-references: 35-40, 1992, 1111-1112, 1113-1114
 A Notes: 1115
 A Importance: 1116
 A Significance: 1117

Query Match	60.0%	Score 362	bits 27	Length 104
Post-Filter Similarity	94.5%	Percent 11		
Matches	62	Conservation	47	Mismatches 27
GC	1	CHROMOSOME	11	
Id	80	CHROMOSOME	90	

RESULT 8

Accession Number: F06987
Source: GenBank
Organism: Streptococcus pneumoniae
Accession Date: 03-Aug-2001
Release Date: 03-Aug-2001
Update Date: 03-Aug-2001
Version: 1

F. J. Beckwith, H. J. Nilsen, K. E. Paulsen, L. J. Eisman, J. A. Reed, L. D. Petersen, S. J. Hedley, J. B. Macnam, L. A. White, and S. Salzberg, S. J. Lewis, M. B. Kattner, and H. H. Haggerty, *Environ. Sci. Technol.* 39, 498-506, 2001.

A Title: *Complete Genome Sequence of a Strain Isolate of Streptococcus parvulus*.
A Reference number: A50500; MIMD:2157209; PMID:11464916
A Revision: A5002
A Status: Preliminary
A Molecular Type: DNA
A Feature: 1 to 2,800
A Feature Features: ORF00572; FIMNAK74379.1; P10314971057; GREEBGN00164; TIGR4
A Experimental Source: Strain: TIGR4
A Genotypes:
A Gene: SP0189

	60-082	North 36	IB 27	Length 142
Qty March				
Best Local Similarity	77.8%			
March 7	Constructive	07	Mismatches	2
			Indels	0
07	1	CHAKIMIN	9	
		11111111		
DB	13	CHAKIMIN	21	

RESULT 9
E97893

Journal of Interpersonal Violence 22(10) 1307-1321
© Association for Prevention of Battering 2007

R-Hoshikawa, J., A. A. Alborn, Jr., W. Arnold, J. Hasegawa, L. Porcelli, S. DeBolt, R. S. O'Keefe, D. J. Lee, E. C. Leckie, E. J. Lee, J. Matsushima, P. McArthur, S. Y. Park, S. M. P. Winkler, M. E. J. Bacteriol. 183, 5709-5717, 2001

Accession: E97893

```

A:Status: preliminary
A:Model: 1300, 2MA
A:Residuals: 1 142 -RUR-
A:Dates: 1997-07-07T07:47:Z; 1997-07-07T07:47:Z; 1997-07-07T07:47:Z
C:Good: 1
A:Good: 1
A:Good: 1

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Query Match	50.0%	Score 35	DB	Length 142
Best Local Similarity	77.8%	Match No. 143		
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07	1	Conservative	9	
	1	1	1	
DB	14	CRKATML	21	

S73104
DNA extracted from poliovirus (D₁, 2-7-76) 111 Large strain R91 Epitopes octacolumnar
C/Spectrum: Epitopes octacolumnar
C/Dated: 15-Feb-1997 #sequence_revision: 27 Feb 1997 #text_change: 07-Nov-1999
#Accession: S73104; S73016
Klein, A.
Submitted to the EMBL Data Library: August 1992

A: Molecule type: DNA
A: Residues: 1-511 <K1P>

Author's Present Address: EMILIO, 77-70, NIT-93315, 1100221562, P.O. Box 1204085,
B. Kaufmann, J.J. Florian, V.J. Klein, A.
Nucleic Acids Res. 20, 5985-5989, 1992

A:11111116A
 A:11111116A
 A:Reference number: S704121
 A:Accession: S70416
 A:Molecule type: DNA
 A:Restriction: 1122-6546

Best Local Similarity 55.68; Pred. No. 14;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CHAKKMLN 9
111111111
Db 15 CHAKKMLN 23

RESULT 15

S29506

neurotensin receptor - human

C1:Species: Homo sapiens (man)

C1:Date: 11-Jan-1995 #sequence_revision 12 Jan 1995 #cdt_change 17-Mar-2000

C1:Accession: S29506

C1:Vital: N.; Laurent, P.; Joly, S.; Chalons, P.; Dumortier, X.; Kiehn, M.; Gilly, D.; Le H

FEMS Lett. 317, 139-142, 1993

A1:Title: Cloning and expression of a complementary DNA encoding a high affinity human ne

A1:Reference number: S29506; M01D:94154505

A1:Accession: S29506

A1>Status: Preliminary

A1:Molecule type: mRNA

A1:Residues: 1-418 -Y112

A1:Cross-references: EMBL:X70070; NID:945020; PDB:CAA49675.1; PIR:435021

C1:Superfamily: vertebrate rhodopsin

C1:Keywords: G protein-coupled receptor; transmembrane protein

Query Match

58.38; Score 35; DH 2; Length 418;

Best Local Similarity 58.38; Pred. No. 60;

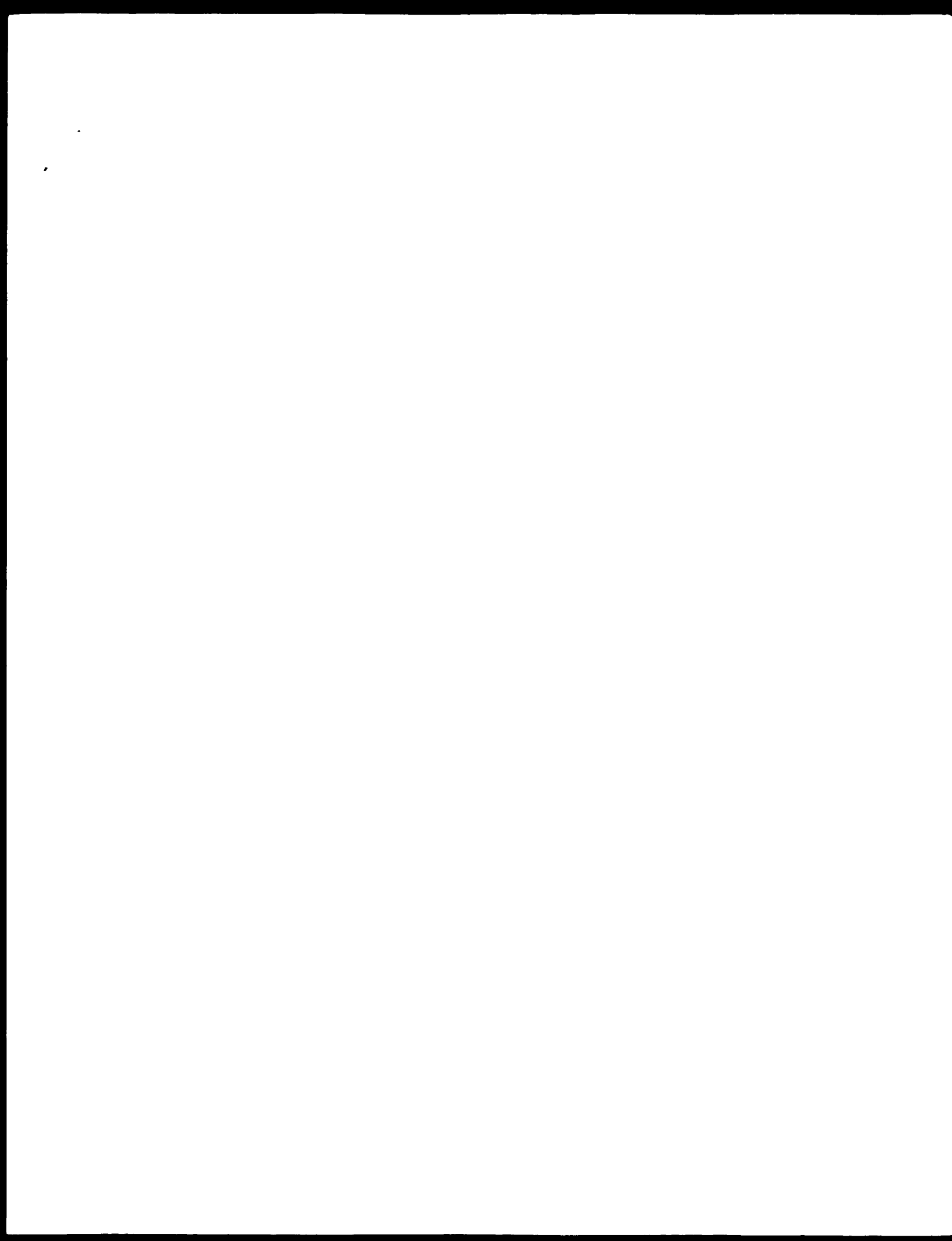
Matches 7; Conservative 3; Mismatches 0; Indels 2; Gaps 1;

OY 1 CH--KAKTMLNR 10

1111111111

Db 171 CHPKAKTLMNR 182

Search completed: July 15, 2002, 14:03:22
Job time: 375 sec



GenCore version 4.1
Copyright (c) 1994 - 2000 Computer Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 14:05:04 : Search time 14.49 seconds

(without alignment)

Title: US-09-719-053a-5

Perfect score: 61

Sequence: 1 CHKAKIMLNRI 11

Scoring table: HIGSJM62

Gapop 10.0 , Gapext 0.5

Search: 105224 seqs, 38719559 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 98

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_407*

Prot. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	39	65.0	470	LEML_BOVIN	prolactin bos (bovines)
2	36	60.0	103	PERH_BOVIN	p47607 prolactin bos (bovines)
3	35	59.3	92	CHRG_MOUSE	chromatin mouse (mus musculus)
4	35	58.3	341	TRPC_MOUSE	transient receptor potential cation channel mouse (mus musculus)
5	35	58.3	418	NTP1_HUMAN	non-templated protein 1 human (homo sapiens)
6	35	58.3	424	NTP1_MOUSE	non-templated protein 1 mouse (mus musculus)
7	35	58.3	424	NTR1_RAT	non-templated protein 1 rat (rattus norvegicus)
8	35	58.3	833	LD_PROMO	LD-promoter human (homo sapiens)
9	35	58.3	844	CNA_KAT	cardiac natriuretic factor human (homo sapiens)
10	35	58.3	867	PROL_IPMA	prolactin porcine (Sus scrofa)
11	35	58.3	866	CRGA_HUMAN	cardiac glycoside resistance gene human (homo sapiens)
12	25	58.3	2339	RPC1_PLAUA	retinol-binding protein 1 placental (Macaca mulatta)
13	34	56.7	179	YPOO_MOUSE	yeast polyoma virus mouse (Mus musculus)
14	34	56.7	403	PBX1_PASTE	polycomb target 1 Pasteur Institute (Homo sapiens)
15	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
16	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
17	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
18	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
19	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
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27	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
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30	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
31	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
32	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
33	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
34	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
35	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
36	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
37	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
38	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
39	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
40	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
41	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
42	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
43	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
44	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
45	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)

Result ID	Score	Match	Length	ID	Description
1	39	65.0	470	LEML_BOVIN	prolactin bos (bovines)
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3	35	59.3	92	CHRG_MOUSE	chromatin mouse (mus musculus)
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6	35	58.3	424	NTP1_MOUSE	non-templated protein 1 mouse (mus musculus)
7	35	58.3	424	NTR1_RAT	non-templated protein 1 rat (rattus norvegicus)
8	35	58.3	833	LD_PROMO	LD-promoter human (homo sapiens)
9	35	58.3	844	CNA_KAT	cardiac natriuretic factor human (homo sapiens)
10	35	58.3	867	PROL_IPMA	prolactin porcine (Sus scrofa)
11	35	58.3	866	CRGA_HUMAN	cardiac glycoside resistance gene human (homo sapiens)
12	25	58.3	2339	RPC1_PLAUA	retinol-binding protein 1 placental (Macaca mulatta)
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31	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
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36	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
37	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
38	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
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43	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
44	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
45	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)

ALIGNMENTS

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24	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
25	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
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30	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
31	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
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44	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)
45	34	56.7	423	V107_MOUSE	von Willebrand factor mouse (Mus musculus)

SMART: SM00042; CITE: 2.
 SMART: SM00044; CITE: 1.
 SMART: SM00181; CITE: 1.
 PROSITE: PS00022; PDB: 1.1.
 PROSITE: PS01186; PDB: 2.1.
 PROSITE: PS00615; CTYPE: LPTN_1.
 PROSITE: PS00041; CTYPE: LPTN_2.
 KW Col1 adhesin; Transmembrane; glycoprotein; EGF-like domain; Location
 KW Selecting Stopcod: Sosh1, pepod
 E SIGNAL 1 24 POTENTIAL.
 E PROPEP 29 48 POTENTIAL.
 E CHAIN 49 73 L-SELECTIN.
 E TRANSFER 44 44 EXTRACELLULAR (POTENTIAL).
 E DOMAIN 45 42 POTENTIAL.
 E DOMAIN 45 155 CYTOPLASMIC (POTENTIAL).
 E DOMAIN 146 192 C-YPE LPTN (SHORT FORM).
 E SIGNAL 1 29 SOSH1 1.
 E DOMAIN 298 417 SOSH1 2.
 E E1S0LFD 52 155 HY SIMILARITY.
 E E1S0LFD 128 147 HY SIMILARITY.
 E E1S0LFD 140 171 HY SIMILARITY.
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 E E1S0LFD 182 191 HY SIMILARITY.
 E E1S0LFD 197 241 HY SIMILARITY.
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 E E1S0LFD 289 416 HY SIMILARITY.
 E CARO-HVD 60 60 N LINKED (GLYCAC. . .) (POTENTIAL).
 E CARO-HVD 77 77 N LINKED (GLYCAC. . .) (POTENTIAL).
 E CARO-HVD 104 104 N LINKED (GLYCAC. . .) (POTENTIAL).
 E CARO-HVD 177 177 N LINKED (GLYCAC. . .) (POTENTIAL).
 E CARO-HVD 216 216 N LINKED (GLYCAC. . .) (POTENTIAL).
 E CARO-HVD 226 226 N LINKED (GLYCAC. . .) (POTENTIAL).
 E CARO-HVD 246 246 N LINKED (GLYCAC. . .) (POTENTIAL).
 E CARO-HVD 408 408 N LINKED (GLYCAC. . .) (POTENTIAL).
 E CARO-HVD 420 420 N LINKED (GLYCAC. . .) (POTENTIAL).
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Query Match Best Local Similarity 65.0%; Score 39; DB 1; Length 470;
 Matches 72; Conservative 0; Pct. No. 4;
 Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

1 CHAKKML 8
 147 CHAKKML 154

RESULT 2
 PRIH ECOLI STANDARD; PRT: 103 AA.
 AV P07015.
 01 APR-1989 (601, 37, created)
 01 MAR-1992 (601, 21, last sequence update)
 16-OCT-2001 (601, 40, last annotation update)
 DE Primosomal replication protein N.
 CN PRIH OR 04201.
 OS Escherichia coli.
 " Bacterial: Proteobacteria; gamma subdivision; Enterobacteriaceae
 " Escherichia.
 "X NBI TaxID 562.
 RN [1]
 SEQUENCE FROM N.A.
 RP MEDLINE 94415507; PubMed 6526756.
 RX "The bacterial sequence of an Escherichia coli chromosomal region
 R1 containing the genes for ribosomal proteins S6, S18, 19 and an open
 R1 reading frame."
 RI Mol. Gen. Genet. 204:126-132(1996).
 RN 121
 RP SEQUENCE FROM N.A.
 RE STRAIN K12 / Hfr1597

RE MEDLINE-95334462; PubMed 7610040;
 RA Portland V.D., Plunkett G., III, Sofia H.J., Daniels D.L.,
 RA Blattner F.R.;
 RI "Analysis of the Escherichia coli genome VII: DNA sequence of the
 RI region from 42.8 through 100 minutes."
 RI Nucleic Acids Res. 23:2195-2199(1995).
 RN [1]
 RP SEQUENCE OF 1, 27, AND FUNCTION.
 RE STRAIN K12.
 RX MEDLINE-91819687; PubMed 2856227;
 RA Zavitz K.H., Blake E.D., Hattias K.J.;
 RI "The pH and pH regulation proteins of Escherichia coli, known
 RI as pKa-regulated overexpression and purification."
 RI J. Biol. Chem. 266:11640-11644(1991).
 RN [4]
 RE SEQUENCE OF 1, 27, AND FUNCTION.
 RX MEDLINE-91260623; PubMed 1646811;
 RA Allen G.C., Jr., Kornberg A.;
 RI "The pH gene encoding the primosomal replication protein of
 RI Escherichia coli."
 RI J. Biol. Chem. 266:11640-11644(1991).
 CC "FUNCTION: RNA DEPENDENT A SPECIFIC HATKIN ENZYME ON THE
 CC SDNA. THIS STRUCTURE IS THEN KETOENZYME AND BIND BY PROTEINS
 CC PRIH AND PRIC. FORMATION OF THE PRIMOSOME PROCEEDS WITH THE
 CC SUBSEQUENT ACTING OF DNA, DNA, DNA AND PRICASE.
 CC "THIS SWISS-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC or send an email to bioinformatics@ebi.ac.uk.
 CC EMBL: X04922; GAT2653.1;
 DR EMBL: 014003; AA597597.1;
 DR EMBL: AF000491; AAC77506.1;
 DR F018 A0281; Q4DCEP.
 DR Ecdosome: F010764; PRIH.
 DR Primosome: Complete proteome.
 KW INIT_MET 0
 SU SEQUENCE 103 AA: 11411 MW: 98A156EA72061D97 GRC044

Query Match Best Local Similarity 60.0%; Score 36; DB 1; Length 103;
 Matches 62; Conservative 3; Pct. No. 4;
 Mismatches 2; Mismatches 2; Indels 0; Gaps 0;

1 CHAKKML 11
 79 CHAKKML 89

RESULT 3
 GIK3 ECOLI STANDARD; PRT: 82 AA.
 AC P37687.
 01-OCT-1994 (601, 40, created)
 01-FEB-1995 (601, 41, last sequence update)
 01-MAR-2002 (601, 41, last annotation update)
 DE Glutaredoxin 3 (GRX3).
 CN GRX3 OR 03610 OR 25037 OR E034488.
 OS Escherichia coli.
 " Bacterial: Proteobacteria; gamma subdivision; Enterobacteriaceae
 " Escherichia.
 "X NBI TaxID 562; 53344;
 RN [1]
 SEQUENCE FROM N.A.
 RP STRAIN K12 / Hfr1597;
 RX MEDLINE 94415507; PubMed 6041620;
 RA Sofia H.J., Portland V.D., Daniels D.L., Blattner F.R.;
 RI "Analysis of the Escherichia coli genome V: DNA sequence of the

01 FEB 1996 (rel. 43; Cited)
02 FEB 1996 (rel. 43; last sequence update)
03 FEB 1996 (rel. 43; last annotation update)
04 FEB 1996 (rel. 43; last annotation update)
05 FEB 1996 (rel. 43; last annotation update)
06 FEB 1996 (rel. 43; last annotation update)
07 FEB 1996 (rel. 43; last annotation update)
08 FEB 1996 (rel. 43; last annotation update)
09 FEB 1996 (rel. 43; last annotation update)
10 FEB 1996 (rel. 43; last annotation update)
11 FEB 1996 (rel. 43; last annotation update)
12 FEB 1996 (rel. 43; last annotation update)
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14 FEB 1996 (rel. 43; last annotation update)
15 FEB 1996 (rel. 43; last annotation update)
16 FEB 1996 (rel. 43; last annotation update)
17 FEB 1996 (rel. 43; last annotation update)
18 FEB 1996 (rel. 43; last annotation update)
19 FEB 1996 (rel. 43; last annotation update)
20 FEB 1996 (rel. 43; last annotation update)
21 FEB 1996 (rel. 43; last annotation update)
22 FEB 1996 (rel. 43; last annotation update)
23 FEB 1996 (rel. 43; last annotation update)
24 FEB 1996 (rel. 43; last annotation update)
25 FEB 1996 (rel. 43; last annotation update)
26 FEB 1996 (rel. 43; last annotation update)
27 FEB 1996 (rel. 43; last annotation update)
28 FEB 1996 (rel. 43; last annotation update)
29 FEB 1996 (rel. 43; last annotation update)
30 FEB 1996 (rel. 43; last annotation update)

06	EMIL2	074455	AAV5081.1		
06	HSNP	1081297	1EJN		
06	101011002	1P000934	See the phosphatase		
06	101011002	1P000939	See the phosphatase		
06	101011002	1P000944	See the phosphatase		
06	SMAR1	SR001566	1P2A7.1		
06	101011002	1P000925	See the phosphatase		
06	KM	Hydrolyase (from Mannose)			
06	ET	MetAl	51	91	IRON (BY SIMILARITY).
06	ET	MetAl	53	53	IRON (BY SIMILARITY).
06	ET	MetAl	79	79	IRON AND MANNANASE (BY SIMILARITY).
06	ET	MetAl	111	111	MANNANASE (BY SIMILARITY).
06	ET	MetAl	112	112	GENERAL AL11 (BY SIMILARITY).
06	ET	MetAl	161	161	MANNANASE (BY SIMILARITY).
06	ET	MetAl	245	245	MANNANASE (BY SIMILARITY).
06	SR001001	FE	403 AA	4400 MW	76080820H20H971A CR5.41

Unit	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Unit	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Unit	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Unit	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Unit	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Unit	1	2	3	4	5	6																																																																																														

Accession	Strain	Year	Ref.
AF017200	Strain 17	1991	17
AF017201	Strain 17	1991	17
AF017202	Strain 17	1991	17
AF017203	Strain 17	1991	17
AF017204	Strain 17	1991	17
AF017205	Strain 17	1991	17
AF017206	Strain 17	1991	17
AF017207	Strain 17	1991	17
AF017208	Strain 17	1991	17
AF017209	Strain 17	1991	17
AF017210	Strain 17	1991	17
AF017211	Strain 17	1991	17
AF017212	Strain 17	1991	17
AF017213	Strain 17	1991	17
AF017214	Strain 17	1991	17
AF017215	Strain 17	1991	17
AF017216	Strain 17	1991	17
AF017217	Strain 17	1991	17
AF017218	Strain 17	1991	17
AF017219	Strain 17	1991	17
AF017220	Strain 17	1991	17
AF017221	Strain 17	1991	17
AF017222	Strain 17	1991	17
AF017223	Strain 17	1991	17
AF017224	Strain 17	1991	17
AF017225	Strain 17	1991	17
AF017226	Strain 17	1991	17
AF017227	Strain 17	1991	17
AF017228	Strain 17	1991	17
AF017229	Strain 17	1991	17
AF017230	Strain 17	1991	17
AF017231	Strain 17	1991	17
AF017232	Strain 17	1991	17
AF017233	Strain 17	1991	17
AF017234	Strain 17	1991	17
AF017235	Strain 17	1991	17
AF017236	Strain 17	1991	17
AF017237	Strain 17	1991	17
AF017238	Strain 17	1991	17
AF017239	Strain 17	1991	17
AF017240	Strain 17	1991	17
AF017241	Strain 17	1991	17
AF017242	Strain 17	1991	17
AF017243	Strain 17	1991	17
AF017244	Strain 17	1991	17
AF017245	Strain 17	1991	17
AF017246	Strain 17	1991	17
AF017247	Strain 17	1991	17
AF017248	Strain 17	1991	17
AF017249	Strain 17	1991	17
AF017250	Strain 17	1991	17
AF017251	Strain 17	1991	17
AF017252	Strain 17	1991	17
AF017253	Strain 17	1991	17
AF017254	Strain 17	1991	17
AF017255	Strain 17	1991	17
AF017256	Strain 17	1991	17
AF017257	Strain 17	1991	17
AF017258	Strain 17	1991	17
AF017259	Strain 17	1991	17
AF017260	Strain 17	1991	17
AF017261	Strain 17	1991	17
AF017262	Strain 17	1991	17
AF017263	Strain 17	1991	17
AF017264	Strain 17	1991	17
AF017265	Strain 17	1991	17
AF017266	Strain 17	1991	17
AF017267	Strain 17	1991	17
AF017268	Strain 17	1991	17
AF017269	Strain 17	1991	17
AF017270	Strain 17	1991	17
AF017271	Strain 17	1991	17
AF017272	Strain 17	1991	17
AF017273	Strain 17	1991	17
AF017274	Strain 17	1991	17
AF017275	Strain 17	1991	17
AF017276	Strain 17	1991	17
AF017277	Strain 17	1991	17
AF017278	Strain 17	1991	17
AF017279	Strain 17	1991	17
AF017280	Strain 17	1991	17
AF017281	Strain 17	1991	17
AF017282	Strain 17		

RL Virology 179:247-266(1990).
 RN [2]
 RP COMPLETIFB GENOME.
 RA "The CompletiFB genome is a 12.5 kb dsDNA virus with a 3.5 kb
 RA "completiFB" gene and a 9.0 kb "completiFB" gene."
 RI "Appendix to 'The CompletiFB genome' of 'Virology 179:247-266(1990)."
 RL Virology 179:247-266(1990).
 CC 1. SIMILARITY: MEMBERS TO THE POLYOMAVIRUS 17 FAMILY.
 CC
 CC
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 CC or send an email to license@isb.ch).
 CC
 CC EMBL: M35027; AAA48053.1;
 DR PIR: G42511; G42511.
 KR Date protein.
 SG Sequence 423 AA; 19039 MW; 6434501637FLH; 33 CRG064;

Only	1	CHAKKIMANI	11	56.7%	Score	44	148	12	Length	4.23
1b	408	CHAKKIMANI	418	111%	Prod. No.	3.22				
Matches	72	Connections	92	Mismatches	41	Index	01	Copies	02	

Search completed: July 15, 2002, 14:05:05
Job time: 348 sec

Genome version 4.5
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EM protein protein search, using sw model

Run on: July 15, 2002, 14:04:44 : Search time 41.38 seconds

(without alignments)
45,987 Million cell updates/sec

Title: US-09-719-053a-5
Percent scores: 6.0
Sequences: 1 (HEAATMENL11)

Scoring table:
Gapop 10.0, Gapext 0.5

Searched: 56222 seqs, 17294329 to slices

Total number of hits satisfying chosen parameters: 56222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_archaea:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_murc:*
8: SP_organellae:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriophage:*
17: SP_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	85.0	213	4	Q9RTZ3
2	51	85.0	244	4	Q9DHY9
3	41	68.3	244	11	Q9DHY9
4	41	68.3	244	11	Q9DHY9
5	41	68.3	244	11	Q9DHY9
6	41	68.3	244	11	Q9DHY9
7	41	68.3	244	11	Q9DHY9
8	41	68.3	244	11	Q9DHY9
9	41	68.3	244	11	Q9DHY9
10	38	64.3	543	5	Q9XZJ1
11	37	61.7	481	5	Q9XZJ1
12	37	61.7	877	5	Q9XZJ1
13	26	40.1	132	16	Q9XZJ2
14	26	40.1	132	16	Q9XZJ2
15	26	40.1	143	2	Q9XZJ2
16	26	40.1	323	16	Q9XZJ2

17	36	60.0	511	5	Q9XZJ2
18	36	60.0	946	10	Q9XZJ2
19	36	60.0	1497	5	Q9XZJ2
20	36	60.0	1571	5	Q9XZJ2
21	36	60.0	1612	5	Q9XZJ2
22	36	58.3	238	4	Q9XZJ2
23	36	58.3	238	4	Q9XZJ2
24	36	58.3	238	4	Q9XZJ2
25	36	58.3	238	4	Q9XZJ2
26	36	58.3	238	4	Q9XZJ2
27	36	58.3	238	4	Q9XZJ2
28	36	58.3	238	4	Q9XZJ2
29	36	58.3	238	4	Q9XZJ2
30	36	58.3	238	4	Q9XZJ2
31	36	58.3	238	4	Q9XZJ2
32	36	58.3	238	4	Q9XZJ2
33	36	58.3	238	4	Q9XZJ2
34	36	58.3	238	4	Q9XZJ2
35	36	58.3	238	4	Q9XZJ2
36	36	58.3	238	4	Q9XZJ2
37	36	58.3	238	4	Q9XZJ2
38	36	58.3	238	4	Q9XZJ2
39	36	58.3	238	4	Q9XZJ2
40	36	58.3	238	4	Q9XZJ2
41	36	58.3	238	4	Q9XZJ2
42	36	58.3	238	4	Q9XZJ2
43	36	58.3	238	4	Q9XZJ2
44	36	58.3	238	4	Q9XZJ2
45	36	58.3	238	4	Q9XZJ2

ALIGNMENTS

RESULT 1	Q9RTZ3	PRELIMINARY:	PKT:	243 AA.
Q9RTZ3	Q9RTZ3	Q9RTZ3	Q9RTZ3	Q9RTZ3
AC	Q9RTZ3	Q9RTZ3	Q9RTZ3	Q9RTZ3
DE	01-JUN-2001 (TEMBL:01, 17, created)			
DE	01-JUN-2001 (TEMBL:01, 17, last sequence update)			
DE	01-DEC-2001 (TEMBL:01, 19, last annotation update)			
DE	HYPOTHETICAL 25.8 KDA PROTEIN (FRAGMENT).			
OS	homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID:9606;			
FN	[1]			
RP	SEQUENCE FROM N.A.			
TC	TISSUE=LUNG CARCINOMA;			
KA	Strasbourg R.			
KB	Submitted (Feb 2001) to the EMBL/GenBank/DBJ databases.			
CC	1-1 SIMILARITY: BELONGS TO THE SHORT-CHAIN HYDROPHASES/REDUCTASES (SDR) FAMILY.			
CC	EMBL: BC001018; AA03018.1; -			
DR	HSSP: P08074; ICYD.			
DR	InterPro: IPR002198; ADL_SHORT.			
DR	Pfam: PF00106; adh_short.1.			
DR	Trinets, Tricob8, SDRADACT.			
DR	PROSITE: PS00061; ADL_SHORT; UNKNOWN_1.			
FT	FUNCTIONAL FROM: oxidoreductase.			
FT	NONTER			
FT	SEQUENCE 213 AA. 2792 MW. Q9RTZ3			

Query Match: 85.0%; Score 51; DB 4; Length 243;
Best Local Similarity: 100.0%; Pred. No. 0.041;
Matches: 10; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0

DB: 194 HEAATMENL1 203

RESULT	6
0920N9	
ID	0920N9
AC	0920N9
DT	01-Dec-2001 (TriMRel: 19, Created)
DT	01-Dec-2001 (TriMRel: 19, Last sequence update)
DT	01-Dec-2001 (TriMRel: 19, Last annotation update)
DE	BLACTYL/L-XYLULOSE FERMENTASE (EC 1.1.1.19, GIR)
GN	
OS	Acetivibrio parvulus (Gillies 1913)
OC	Elkayariota: Methylozo: Chordata: Graptaria: Vertebrata: Euteleostomi: Actinopterygii: Cyprinodontiformes: Poeciliidae: Poecilia
NC	Elkayariota: Methylozo: Chordata: Graptaria: Vertebrata: Euteleostomi: Actinopterygii: Cyprinodontiformes: Poeciliidae: Poecilia
OX	NCBI_TaxID=101412
GN	111

RESULT	8	
1966090		
19	9360709	PRIMER:NAAT; PR: 740 AA.
AC	p960909;	
DI	01-MAY-1997 (TREMBLrel. 03, Created)	
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)	
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE	BEFA-Xylo-OLIGOSYLASE.	
GN	XLS.	
OS	Thermotogaobacter boeckii (Thermotogaobium boeckii).	
OC	Bacteriia; Firmicutes; Bacilli/Thiosulfibacter group;	
OC	Thermotogaobacter group; Thermotogaobacter.	
OX	111_24316.29423;	
OX	111	
SE	SEQUENCE FROM N.A.	
SP	BEHLIND 9248447; PMID 92287944;	
KA	Accession K; Progenomicro K; Wild N; Standardizer W.L..	
KA	Bohemianist J..	
IT	"Genes classified into different taxa plus analysis of the microarray data for boeckii are clustered in a common operon."	
MT	Appl. Environ. Microbiol. 65:1992-1999(1997).	

	RESULT	13
099XPZ		
ID	O6XK79	FPELIMNAVY.
AN	Q9GXPZ	PRT. 132 AA.
D1	01-JUN-2001 (TEMBUROL_17) (revised)	
D2	01-JUN-2001 (TEMBUROL_17) last sequence update)	
D3	01-DEC-2001 (TEMBUROL_19) last annotation update)	
D4	HYPOTHETICAL PROTEIN SPV2115.	
DN	SPV2115	
OS	Streptococcus pyogenes.	
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;	
CC	Streptococcus.	
OX	NCBI_TaxID:1314;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN SE370 / ATCC 700294 / SEROTYPE M1:	
RX	MEDLINE: 21192484; PubMed: 11292296;	
RA	FERRICCI J.D., Meshkin W.H., Aldrich R.C., Saito D., Smith G., Zhou K.,	
RA	Frimanek R.E., Seayad S., Stropov A.N., Kenton S., Lai H.S., Lin S.P.,	
RA	Qian Y., Jia H.G., Najjar F.Z., Ron G., Zhu H., Good L.,	
RA	Yuan X., Gilton S.W., Koop R.A., McLaughlin R.J.	
R1	"Complete genome sequence of an M1 strain of <i>Streptococcus pyogenes</i> ."	
R2	Proc. Natl. Acad. Sci. U.S.A. 98(46):4653(2001).	
RL	EMBL: AF006631; AKK34760.1; -	
RW	Hypothetical protein; Complete genome.	
S2	SPV2115PRT. 132 AA. 1700388, 3538221AACTACTGGTCA	

	Seq. ID	Score 66	148	1.56	1.56	1.56
	Post Local Similarity	77.80%				
	Matches	72	Conservation	0%	Mismatches	2%
QY	1 CHIKAKTEN 9					
	1 1 1 1 1 1					
DB	13 CHIKAKTEN 21					

RESULT	15	
Q9R039		
ID	Q9R039	PRELIMINARY; PRZ: 143 AA.
AC	Q9R039;	
DT	01-MAY-2000 (RELEASE)	13, Created)
ET	01-MAY-2000 (RELEASE)	13, last sequence update)
DI	01-JUN-2001 (RELEASE)	17, last annotation update)
DE	CP89H (FRAGMENT).	
GN	CP89H.	
SS	Streptococcus suis.	
LC	bioRxiv: Streptococcus, Bacillus/Enteridium group; Streptococcus?	
GC	Streptococcus.	
EX	NCBI:1a4D-1407?	
EN	111	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-5218;	
EX	MEDLINE:99184998; PubMed=10085014;	
FA	Smith H.E., Duncan M., van der Velde J., Weerman P., Wisselink H.J.,	
RA	et al. Koele Zoonoosch N., Smiths M.A.:	
RI	"Identification and characterization of the cps locus of Streptococcus	
RI	suis serotype 2: The capsule protects against phagocytosis and is an	
RI	important virulence factor."?	
RL	Infect. Immun. 67:1750-1756(1999).	
LN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN 5218;	
EX	MEDLINE:99419140; PubMed 1048466;	
FA	Smith H.E., Weerman P., van der Velde J., Weerman P.,	
RA	Wisselink H.J., Smiths M.A.:	
RI	"The cps genes of Streptococcus suis serotypes 1, 2, and 9:	

RT development of TaqI seed for specific PCR assays:
 BL J. Clin. Microbiol. 37:4146-4152(1999).
 DR EMBOJ. 26:155805; AAF18951.1; -;
 DR InterPro: IPR00173; Glycos_transf_2.
 DR Pfam: PF00535; Glycos_transf_2; 1.
 ET NCBI TER 143 143
 SE SEQUENCE 143 AA; 15445 MW; 011A9D443200860 CDS64;

Query Match: 60.0%; Score 46; DR 2; Length 143;
 Post local Similarity 75.0%; Prod. No. 18;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CHKAETMLR
 1111111
 bb 97 CHKAETMLR 104

Search completed: July 15, 2002, 14:04:46
 Job time: 354 sec

Genome version 4.5
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OM protein search, using sw model

Run on: July 15, 2002, 14:58:46 ; Search time of 1.22 seconds

2.6.6.6. *Milvina*

Title:	US-19-719-053A-5
Part of score:	611

CONTENTS

Scoring table: PLUMAZ

Source: 747114 covers 11072766

Total number of birds culled for obvious reasons at each site

Minimum lb ear length = 0

Maximum Likelihood Estimation

Post-Processing: Minimum Match 0.8

Listed first 45 summaries

Attachment : A_01101901_022002_*

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	

Prod. No. is the number of results produced by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result	Score	Query	length	DB	ID	Footprint
1	51	85.0	53	22	AA576102	Human scapula cartilage
2	51	85.0	88	22	AA810195	Human scapula cartilage
3	51	85.0	88	22	AA923032	Human scapula cartilage
4	51	85.0	88	22	AA118406	Human scapula cartilage
5	51	85.0	122	22	AA576265	Human scapula cartilage
6	51	85.0	122	22	AA576081	Human scapula cartilage
7	51	85.0	134	21	AA543805	Human scapula cartilage
8	51	85.0	244	20	AA543807	Human scapula cartilage
9	51	85.0	244	22	AA579215	Human scapula cartilage
10	51	85.0	244	21	AA579216	Human scapula cartilage
11	51	85.0	254	22	AA010254	Human scapula cartilage

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80																				

ALLEGMENTS

RESULT

1.0 AU₂₈₀ standard; Protein; 53 AU

616 *Y. Y.*

First Entry

47. 2000. *Journal of the American Veterinary Medical Association* 268:666.

W. B. and J. C. are grateful to the National Science Foundation for support of this work.

X

05-043-50
XX

XX
XX
36-680-20000-200000-1000000XX
XX
00-0100-1000-0000-0167137

PR 03-NOV-1999; 99JUS-0163280

17A (HUGA) HUMAN GENOME SCI INC

P1 Ruben SM, Harash SO, Hirse GE, Rosen CA;

MR. WILSON: 2001-2002/24.
MR. WILSON: 2001-2002/24.
MR. WILSON: 2001-2002/24.

X

For $\alpha \in \mathbb{R}$, let \mathcal{H}_α denote the Hilbert space of functions f on \mathbb{R}^d with norm

08-N-V-2000; 2560MS-246475P.
PR 08-N-V-2000; 2560MS-246476P.
PR 08-N-V-2000; 2560MS-246477P.
PR 08-N-V-2000; 2560MS-246478P.
PR 08-N-V-2000; 2560MS-246524P.
PR 08-N-V-2000; 2560MS-246524P.
PR 08-N-V-2000; 2560MS-246525P.
PR 08-N-V-2000; 2560MS-246526P.
PR 08-N-V-2000; 2560MS-246527P.
PR 08-N-V-2000; 2560MS-246528P.
PR 08-N-V-2000; 2560MS-246532P.
PR 08-N-V-2000; 2560MS-246609P.
PR 08-N-V-2000; 2560MS-246610P.
PR 08-N-V-2000; 2560MS-246611P.
PR 08-N-V-2000; 2560MS-246613P.
PR 17-N-V-2000; 2560MS-249207P.
PR 17-N-V-2000; 2560MS-249208P.
PR 17-N-V-2000; 2560MS-249210P.
PR 17-N-V-2000; 2560MS-249211P.
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PR 17-N-V-2000; 2560MS-249216P.
PR 17-N-V-2000; 2560MS-249217P.
PR 17-N-V-2000; 2560MS-249218P.
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PR 17-N-V-2000; 2560MS-249245P.
PR 17-N-V-2000; 2560MS-249246P.
PR 17-N-V-2000; 2560MS-249254P.
PR 17-N-V-2000; 2560MS-249257P.
PR 17-N-V-2000; 2560MS-249259P.
PR 17-N-V-2000; 2560MS-249260P.
PR 01-DRC-2000; 2560MS-250340P.
PR 01-DRC-2000; 2560MS-250341P.
PR 05-DRC-2000; 2560MS-251030P.
PR 05-DRC-2000; 2560MS-251988P.
PR 05-DRC-2000; 2560MS-256719P.
PR 06-DRC-2000; 2560MS-251779P.
PR 08-DRC-2000; 2560MS-251856P.
PR 08-DRC-2000; 2560MS-251857P.
PR 08-DRC-2000; 2560MS-251858P.
PR 08-DRC-2000; 2560MS-251984P.
PR 08-DRC-2000; 2560MS-251986P.
PR 11-DRC-2000; 2560MS-254997P.
PR 05-JAN-2001; 2560MS-259678P.

(HUMAN) HUMAN CCR-ME-201 INT.

Rosen CA, Parasc SF, Paden SM;
WPI: 2001 476165 ZC1,
N-PSIB; ABA064171.

Isolated nucleic acid molecule encoding an inflammatory associated
polypeptide is used in prevention, treatment or amelioration of said
condition -

Claim 11: SEQ ID NO: 503; 85kbp + Sequence Listing: English.

The present invention provides human CCRMs, proteins and related atoms,
DNAs. These can be used in the treatment of neuronal immune system,
molecular reproductive, cardiovascular, pulmonary, renal vascular,
renal and proliferative disorders and inflammation. The present sequence
is a protein of the invention.

Sequence 88 AA:

Query Match	65.08; 50.00; 51.76; 42.86; 40.00; 33.33; 30.00; 25.00; 20.00; 16.67; 14.29; 12.50; 11.11; 10.00; 9.09; 8.33; 7.69; 7.14; 6.67; 6.25; 5.88; 5.56; 5.26; 5.00; 4.76; 4.55; 4.35; 4.17; 4.00; 3.85; 3.70; 3.57; 3.45; 3.33; 3.23; 3.13; 3.03; 2.94; 2.86; 2.78; 2.70; 2.63; 2.56; 2.50; 2.44; 2.38; 2.33; 2.27; 2.22; 2.17; 2.13; 2.08; 2.04; 2.00; 1.96; 1.92; 1.89; 1.86; 1.83; 1.80; 1.77; 1.74; 1.71; 1.68; 1.65; 1.63; 1.60; 1.58; 1.56; 1.54; 1.52; 1.50; 1.48; 1.46; 1.44; 1.42; 1.40; 1.38; 1.36; 1.35; 1.33; 1.31; 1.29; 1.27; 1.25; 1.23; 1.21; 1.19; 1.17; 1.15; 1.13; 1.11; 1.09; 1.07; 1.05; 1.03; 1.01; 1.00; 0.98; 0.96; 0.94; 0.92; 0.90; 0.88; 0.86; 0.84; 0.82; 0.80; 0.78; 0.76; 0.74; 0.72; 0.70; 0.68; 0.66; 0.64; 0.62; 0.60; 0.58; 0.56; 0.54; 0.52; 0.50; 0.48; 0.46; 0.44; 0.42; 0.40; 0.38; 0.36; 0.35; 0.33; 0.31; 0.29; 0.27; 0.25; 0.23; 0.21; 0.19; 0.17; 0.15; 0.13; 0.11; 0.09; 0.07; 0.05; 0.03; 0.01; 0.00
Host Data, Similarity	100.00; Prod. Mo. 1.00; 0.99; 0.98; 0.97; 0.96; 0.95; 0.94; 0.93; 0.92; 0.91; 0.90; 0.89; 0.88; 0.87; 0.86; 0.85; 0.84; 0.83; 0.82; 0.81; 0.80; 0.79; 0.78; 0.77; 0.76; 0.75; 0.74; 0.73; 0.72; 0.71; 0.70; 0.69; 0.68; 0.67; 0.66; 0.65; 0.64; 0.63; 0.62; 0.61; 0.60; 0.59; 0.58; 0.57; 0.56; 0.55; 0.54; 0.53; 0.52; 0.51; 0.50; 0.49; 0.48; 0.47; 0.46; 0.45; 0.44; 0.43; 0.42; 0.41; 0.40; 0.39; 0.38; 0.37; 0.36; 0.35; 0.34; 0.33; 0.32; 0.31; 0.30; 0.29; 0.28; 0.27; 0.26; 0.25; 0.24; 0.23; 0.22; 0.21; 0.20; 0.19; 0.18; 0.17; 0.16; 0.15; 0.14; 0.13; 0.12; 0.11; 0.10; 0.09; 0.08; 0.07; 0.06; 0.05; 0.04; 0.03; 0.02; 0.01; 0.00
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY		2 HKAKMENR	11
Ldb		74 HKAKMINTI	MZ
RESULT	4		
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ID	AADZ4044 standard, Protein, 86 AA.		
XX			
AC	AADZ4044:		
XX			
DT	17-Dec-2001 (first entry)		
DE	Nicotinamide nucleotide phosphorylase #19.		
XX			
KK	Blood, oxidoreductase enzyme, Transketolase hydrolase; lysine isomerase;		
KM	Hypoxanthine phosphoribosyl transferase deficiency; immunodeficiency disorder;		
KL	autosomal recessive disorder; hypoglycemia at birth; metabolic disorders;		
FW	and hematologic disease; low blood glucose levels; hepatomegaly disorder;		
KW	blood related disorders; infectious disorders; glycolysis; anti arthritis;		
RW	hypophosphorylation; anticonvulsant.		
OS			
XS	Human sapiens.		
XX			
PB	WU200155401-A2.		
XX			
CT	G2 AUG 2001.		
XX			
FT	17 JAN 2001, 2001WO USG230,		
XX			
FR	31 JAN 2000; 2000US-0179065,		
FR	04 FEB 2000; 2000US-0180620,		
FR	24 FEB 2000; 2000US-0184604,		
FR	02 MAR 2000; 2000US-0186350,		
FE	16 MAY 2000; 2000US-0189924,		
FR	17 MAR 2000; 2000US-0190976,		
FR	18 APR 2000; 2000US-0198124,		
FR	19 MAY 2000; 2000US-0205515,		
FR	07 JUN 2000; 2000US-0209467,		
FR	28 JUN 2000; 2000US-0214886,		
FR	30 JUN 2000; 2000US-0215145,		
FR	07 JUL 2000; 2000US-0216647,		
FR	07 JUL 2000; 2000US-0216880,		
FR	11 JUL 2000; 2000US-0217487,		
FR	11 JUL 2000; 2000US-0217496,		
PR	14 JUL 2000; 2000US-0218290,		
PR	26 JUL 2000; 2000US-0220966,		
FR	26 JUL 2000; 2000US-0220964,		
FR	14 AUG 2000; 2000US-0224518,		
FR	14 AUG 2000; 2000US-0224519,		
FR	14 AUG 2000; 2000US-0225214,		
PR	14 AUG 2000; 2000US-0225214,		
PR	14 AUG 2000; 2000US-0225266,		
PR	14 AUG 2000; 2000US-0225267,		
FR	14 AIG 2000; 2000US-0225266,		
FR	14 AIG 2000; 2000US-0225270,		
FR	14 AIG 2000; 2000US-0225447,		
FR	14 AIG 2000; 2000US-0225757,		
FR	14 AIG 2000; 2000US-0225758,		
FR	14 AIG 2000; 2000US-0225759,		
FR	14 AUG 2000; 2000US-0226279,		
FR	14 AUG 2000; 2000US-0226681,		
FR	22 AUG 2000; 2000US-0228586,		
FR	22 AUG 2000; 2000US-0227182,		
FR	24 AUG 2000; 2000US-0227182,		
FR	30 AUG 2000; 2000US-0228924,		
FR	31 SEP 2000; 2000US-0229287,		
FR	01 SEP 2000; 2000US-0229344,		
FR	01 SEP 2000; 2000US-0229344,		
FR	01 SEP 2000; 2000US-0229344,		
FR	05 SEP 2000; 2000US-0229514,		

[illegible][illegible]

[illegible]

(HUMAN) HUMAN GENOME SCL INC.

KOSCIUSKO, PA., KARLASH ST., BOKER EM;
WHL; 2001 6979 6748.
N PDBID: AASZ9576.

Isolated polypeptide for treating, preventing and/or prophylaxis disorders of the endocrine system such as reproductive disorders, endocrine cancers and also for testing and detection e.g. diagnosis claim 11; SEQ ID NO 602; 603PPI Finalish.

Sequences AAU1B2R2-AAU1B2G7 represent endocrine polypeptides of the invention. Endocrine polypeptides and their associated polymorphoids are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by determining the presence or absence of a mutation in an endocrine polypeptide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms, endocrinopathies or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cerebral ischemia, nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, cellular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as Crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as asthma. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotherapy. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. Other: The sequence data for this patent did not form part of the printed

or Specification, but was obtained in elos route format directly from WIT:
 or of 11p.wipo.int/pub/published_for_sequences:

Query Match

65.08; Score 51; 146 22; Length 200;

Best Local Similarity 100.08; P-rod. No. 0.14;

Matches 10; conserved 170; of Mismatches 0; Indels 0; Gaps 0;

QY 2 HAKMINI 11

1-1111111

DB 199 HAKMINI 204

Search completed: July 15, 2002, 14:58:47
 Job time: 440 Sec

Matches 92 Conserved 02 Mismatches 13 Indels 02 Gaps 02

2 HIRAKIMINKI 11
111111111
195 HIRAKIMINKI 204

RESULT 2
US-09-719-053a-14
Sequence 14, Application US-09-719-053a-14
Patent No. 5608025
GENERAL INFORMATION:
APPLICANT: Todd, Thomas F.
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIA TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patented in Release #1.0, Version #1.8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09-07719-053a
FILING DATE: 16 Nov 1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09-07719-053a
FILING DATE: 25 JAN 1994
ATTORNEY/AGENT INFORMATION:
NAME: GUNDELSON, Lino
REGISTRATION NUMBER: 48,479
REFERENCE/SEQUENCE NUMBER: 09-104-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-0000
TELEFAX: 212-596-0000
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
Topology: linear
MULTIPLE TYPE: protein
US-09-719-053a-14

2009 Match 45.0% Score 49.0% Ident 11.0%
Host local Similarity 47.5% Prod. No. 2.6%
Matches 72 Conserved 02 Mismatches 13 Indels 02 Gaps 02

1 HIRAKIMINKI 11
111111111
199 HIRAKIMINKI 116

RESULT 4
US-09-719-053a-21
Sequence 21, Application US-09-719-053a-21
GENERAL INFORMATION:
APPLICANT: Murphy, Michael B.
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MURPHY, Michael B.
STREET: 20004
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIA TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patented in Release #1.0, Version #1.8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09-07719-053a
FILING DATE: 10 SEP 1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09-07719-053a
FILING DATE: 10 SEP 1994

ADDRESSEE: MURPHY, Michael B.
STREET: 20004
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIA TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patented in Release #1.0, Version #1.8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09-07719-053a
FILING DATE: 10 SEP 1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09-07719-053a
FILING DATE: 10 SEP 1994

US-09-719-053a-21
Sequence 21, Application US-09-719-053a-21
Patent No. 5608025
GENERAL INFORMATION:
APPLICANT: Murphy, Michael B.
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MURPHY, Michael B.
STREET: 20004
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIA TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patented in Release #1.0, Version #1.8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09-07719-053a
FILING DATE: 10 SEP 1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09-07719-053a
FILING DATE: 10 SEP 1994

2009 Match 45.0% Score 49.0% Ident 11.0%
Host local Similarity 47.5% Prod. No. 2.6%
Matches 72 Conserved 02 Mismatches 13 Indels 02 Gaps 02

1 HIRAKIMINKI 11
111111111
199 HIRAKIMINKI 116

RESULT 4
US-09-719-053a-21
Sequence 21, Application US-09-719-053a-21
Patent No. 5608025
GENERAL INFORMATION:
APPLICANT: Murphy, Michael B.
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MURPHY, Michael B.
STREET: 20004
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIA TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patented in Release #1.0, Version #1.8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09-07719-053a
FILING DATE: 10 SEP 1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09-07719-053a
FILING DATE: 10 SEP 1994

ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.
 REGISTRATION NUMBER: 34,033
 REFERENCE/OTHER NUMBER: MURPHY 2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-747-4528
 TELEX: 248643
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 453 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-118-279-45

Query Match 58.38% Score 352 DB 12 Length 453
 Host Local Similarity 59.3% Prod No 412
 Matches 7: Conservative 3: Mismatches 0: Indels 2: Gaps 1:

QY 1 CR-KAKMLNR 10
 II 1111111
 DB 105 DKPKMLMSR 116

RESULT 5
 US-0893-08528-45
 Sequence 45, Application PC/PIPS 08528
 GENERAL INFORMATION:
 APPLICANT: New York University
 TITLE OF INVENTION: POLYPEPTIDES OF G COILED PROTEIN
 NUMBER OF SEQUENCES: 448
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROOKLYN AND MIDTOWN
 STREET: 419 Seventh Street, N.W., Suite 400
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS 5.0
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/06872
 FILING DATE: 09-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 05-07-043,236
 FILING DATE: 10-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.
 REGISTRATION NUMBER: 34,033
 REFERENCE/OTHER NUMBER: MURPHY=2 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-747-4528
 TELEX: 248643
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 453 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-0893-08528-45

Query Mat 10 58.38% Score 352 DB 52 Length 453
 Host Local Similarity 58.9% Prod. No. 412

Matches 7: Conservative 3: Mismatches 0: Indels 2: Gaps 1:
 QY 1 CR-KAKMLNR 10
 II 1111111
 DB 105 DKPKMLMSR 116

RESULT 6
 US-08 474-479C-86
 Sequence 86, Application US/08474479C
 Patent No. 5977305
 GENERAL INFORMATION:
 APPLICANT: Michael H.
 TITLE OF INVENTION: GLUTEN BY HYDROLYZATION AND RELATED
 NUMBER OF SEQUENCES: 88
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Looney, Gerstein, Murray & Borun
 STREET: 333 South Wacker Drive, Suite 400
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.00
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,479C
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: A45
 PCT APPLICATION DATA:
 APPLICATION NUMBER: US 07/511,715
 FILING DATE: 28 APR 1990
 PCT APPLICATION DATA:
 APPLICATION NUMBER: US 08/206,188
 FILING DATE: 01-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/688,452
 FILING DATE: 19-APR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Cloud, David W.
 REGISTRATION NUMBER: 36,107
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (412) 474-6300
 TELEFAX: (412) 474-0448
 INFORMATION FOR SEQ ID NO: 86:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 398 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08 474-479C-86

Query Match 58.38% Score 352 DB 22 Length 398
 Host Local Similarity 77.8% Prod. No. 462
 Matches 7: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

QY 2 DKAKMLNR 10
 II 1111111
 DB 109 DKPKMLMSR 117

RESULT 7
 US-07-688 452C-22
 Sequence 22, Application US/07688452C
 Patent No. 5527896
 GENERAL INFORMATION:
 APPLICANT: Widler, Michael H.

1 APPLICANT: Colwell, John J.
 2 TITLE OF INVENTION: Related by Complementat ion and Related
 3 NUMBER OF SEQUENCES: 47
 4 CORRESPONDENCE ADDRESS:
 5 APPLICANT: Marshfield, Charles, Gregory A.
 6 ADDRESS: Marshfield, Charles, Gregory A.
 7 STREET: Two First National Plaza, 20 South Clark
 8 STREET: Street
 9 CITY: Chicago
 10 STATE: Illinois
 11 COUNTRY: USA
 12 ZIP: 60604
 13 COMPUTER RELEVABLE FORM:
 14 MEDIUM TYPE: floppy disk
 15 OPERATING SYSTEM: pc compatible
 16 SOFTWARE: Patent Release #1.0, Version #1.25
 17 CURRENT APPLICATION DATA:
 18 APPLICATION NUMBER: 09/075111
 19 FILING DATE: 20 Apr 1990
 20 PRIORITY/DATE: 20 Apr 1990
 21 NAME: Michael E.
 22 REGISTRATION NUMBER: 25447
 23 REFERENCE/SEQUENCE NUMBER: 2905/00197
 24 TELECOMMUNICATION INFORMATION:
 25 TELEPHONE: (412) 646-5750
 26 TELEFAX: (412) 646-9740
 27 TELE: 25 6064
 28 INFORMATION FOR SEQ ID NO: 22:
 29 SEQUENCE CHARACTERISTICS:
 30 LENGTH: 648 amino acids
 31 TYPE: AMINO ACID
 32 FEATURE: 11000
 33 MOLECULE TYPE: protein
 34 US-07-689-062-22
 35
 36 COPY MATCH 58.8% SCORE 651 DB 12 Length 648
 37 Best Local Similarity 77.8% Prod. No. 721
 38 Matches 71 Conserved 02 Mismatches 21 Indels 02 Gaps 02
 39
 40 2 BREAKLINE 10
 41 11 1111
 42 DB 13 BREAKLINE 21

1 RESULT 8
 2 US-09-942-5218-9
 3 Sequence 9, Application US/089425218
 4 Patent No. 5942477
 5 GENERAL INFORMATION:
 6 APPLICANT: Marshfield, Charles P.
 7 APPLICANT: Marshfield, Charles P.
 8 TITLE OF INVENTION: Human Brain Phosphodiesterase
 9 NUMBER OF SEQUENCES: 9
 10 CORRESPONDENCE ADDRESS:
 11 ADDRESS: Southlake, Beecham Corporation
 12 STREET: Corporate Center 2, P.O. Box 1099
 13 CITY: Kind of Process
 14 STATE: TX
 15 COUNTRY: USA
 16 ZIP: 76066
 17 COMPUTER RELEVABLE FORM:
 18 MEDIUM TYPE: floppy disk
 19 OPERATING SYSTEM: pc compatible
 20 SOFTWARE: Patent Release #1.0, Version #1.25

1 CURRENT APPLICATION DATA:
 2 APPLICATION NUMBER: 09/075111
 3 FILING DATE: October 2, 1997
 4 CLASSIFICATION: 536
 5 PRIOR APPLICATION DATA:
 6 APPLICATION NUMBER: 09/0446, 886
 7 FILING DATE: 22 May 1995
 8 CLASSIFICATION: 536
 9 PRIOR APPLICATION DATA:
 10 APPLICATION NUMBER: 09/029, 464
 11 FILING DATE: 10 March 1993
 12 CLASSIFICATION: 536
 13 PRIORITY/DATE: 10 March 1993
 14 NAME: Marshfield, Charles P.
 15 REGISTRATION NUMBER: 41,824
 16 REFERENCE/SEQUENCE NUMBER: 15014501FW
 17 TELEPHONE: (415) 270-6009
 18 TELEFAX: (415) 270-6009
 19 INFORMATION FOR SEQ ID NO: 9:
 20 SEQUENCE CHARACTERISTICS:
 21 LENGTH: 696 amino acids
 22 TYPE: amino acid
 23 FEATURE: 11000
 24 MOLECULE TYPE: protein
 25 US-09-942-5218-9

1 COPY MATCH 58.8% SCORE 651 DB 12 Length 648
 2 Best Local Similarity 77.8% Prod. No. 721
 3 Matches 71 Conserved 02 Mismatches 21 Indels 02 Gaps 02

1 RESULT 9
 2 US-09-146-249A-85
 3 Sequence 65, Application US/07146249A
 4 Patent No. 6069240
 5 GENERAL INFORMATION:
 6 APPLICANT: Marshfield, Charles P.
 7 APPLICANT: Marshfield, Charles P.
 8 TITLE OF INVENTION: Related by Complementat ion and Related
 9 NUMBER OF SEQUENCES: 85
 10 CORRESPONDENCE ADDRESS:
 11 ADDRESS: Marshfield, Charles, Gregory A.
 12 STREET: Two First National Plaza, 20 South Clark
 13 CITY: Chicago
 14 STATE: Illinois
 15 COUNTRY: USA
 16 ZIP: 60604
 17 COMPUTER RELEVABLE FORM:
 18 MEDIUM TYPE: floppy disk
 19 OPERATING SYSTEM: pc compatible
 20 SOFTWARE: Patent Release #1.0, Version #1.25
 21 CURRENT APPLICATION DATA:
 22 APPLICATION NUMBER: 09/097445, 249A
 23 FILING DATE:
 24 CLASSIFICATION:
 25 PRIORITY/DATE: 20 Apr 1990
 26 NAME: Marshfield, Charles P.
 27 REGISTRATION NUMBER: 41,824
 28 REFERENCE/SEQUENCE NUMBER: 15014501FW
 29 TELEPHONE: (415) 270-6009
 30 TELEFAX: (415) 270-6009
 31 INFORMATION FOR SEQ ID NO: 65:
 32 SEQUENCE CHARACTERISTICS:
 33 LENGTH: 25 amino acids
 34 TYPE: amino acid
 35 FEATURE: 11000
 36 MOLECULE TYPE: protein
 37 US-09-146-249A-85

1 INFORMATION FOR SEQ ID NO: 85:
 2 SEQUENCE CHARACTERISTICS:
 3 LENGTH: 744 amino acids
 4 TYPE: amino acid
 5 TOPOLOGY: linear
 6 MOLECULE TYPE: protein
 7 FEATURES:
 8 NAME/KEY: misc_feature
 9 OTHER INFORMATION: 744 aa protein, secreted, 1-744 aa
 10 Patent No. 6009240
 11 OTHER INFORMATION: acids 152-885 of SEQ ID NO:42 which begins immediately after
 12 OTHER INFORMATION: codon. Stop codon may be in an intron."
 13 US-09-146-219A-85

Query Match 58.3% Score 45; DB 3; Length 744;
 Host Local Similarity 77.8% Prod. No. 83
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 2 BREAKING 10
 1 1 1 1 1
 DB 109 BREAKING 117

RESULT 10
 1 US-08-206-188B-85
 2 Sequence 85, Application US/08206188B
 3 Patent No. 6100026
 4 GENERAL INFORMATION:
 5 APPLICANT: Waltek, Michael H.
 6 APPLICANT: Colicelli, John J.
 7 TITLE OF INVENTION: Cloning by Complementatlon and Related
 8 TITLE OF INVENTION: Processes
 9 NUMBER OF SEQUENCES: 84
 10 CORRESPONDENCE ADDRESS:
 11 ADDRESS: Marshall, Ofc/colic, Gortstein, Murray & Baum
 12 STREET: 6400 Sears Tower, 200 South Wacker Drive
 13 CITY: Chicago
 14 STATE: Illinois
 15 COUNTRY: United States of America
 16 FIP: 6000-0402
 17 COMPUTER READABLE FORM:
 18 MEDIUM TYPE: floppy disk
 19 COMPUTER: IBM PC compatible
 20 OPERATING SYSTEM: PC-DOS/MS-DOS
 21 SOFTWARE: Patent in Release #1.0, Version #1.25
 22 CURRENT APPLICATION DATA:
 23 APPLICATING NUMBER: 02/09/2006/188B
 24 FILING DATE: 01-MAR-1994
 25 CLASSIFICATION: 435
 26 PRIOR APPLICATION DATA:
 27 APPLICATION NUMBER: 05-07/511,715
 28 FILING DATE: 20-APR-1990
 29 ATTORNEY/AGENT INFORMATION:
 30 NAME: Clough, David W.
 31 REGISTRATION NUMBER: 36107
 32 TELECOMMUNICATION INFORMATION:
 33 TELEPHONE: 412/474-6300
 34 TELEFAX: 412 474-0448
 35 TELEEX: 25-4856
 36 INFORMATION FOR SEQ ID NO: 85:
 37 SEQUENCE CHARACTERISTICS:
 38 LENGTH: 744 amino acids
 39 TYPE: amino acid
 40 TOPOLOGY: linear
 41 MOLECULE TYPE: protein
 42 FEATURES:
 43 NAME/KEY: misc_feature
 44 OTHER INFORMATION: 744 aa protein, secreted, 1-744 aa
 45 Patent No. 6100026
 46 OTHER INFORMATION: 152-885 of SEQ ID NO:42 which begins immediately after the
 47 OTHER INFORMATION: stop codon. Stop codon may be in an intron."
 48 US-08-206-188B-85

Query Match 58.4% Score 35; DB 4; Length 744;
 Host Local Similarity 77.8% Prod. No. 83
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 2 BREAKING 10
 1 1 1 1 1
 DB 109 BREAKING 117

RESULT 11
 1 US-08-872-855-11
 2 Sequence 11, Application US/08872855
 3 Patent No. 6121046
 4 GENERAL INFORMATION:
 5 APPLICANT: McCarthy, Sean
 6 APPLICANT: Gearing, David
 7 TITLE OF INVENTION: NEURAL HUMAN DELTA3 COMPOSITIONS AND
 8 TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
 9 NUMBER OF SEQUENCES: 24
 10 CORRESPONDENCE ADDRESS:
 11 ADDRESS: POLEY, HOAG & ELIOT LLP
 12 STREET: One Post Office Square
 13 CITY: Boston
 14 STATE: MA
 15 COUNTRY: USA
 16 FIP: 02189 2170
 17 COMPUTER READABLE FORM:
 18 MEDIUM TYPE: floppy disk
 19 COMPUTER: IBM PC compatible
 20 OPERATING SYSTEM: PC-DOS/MS-DOS
 21 SOFTWARE: Patent in Release #1.0, Version #1.40
 22 CURRENT APPLICATION DATA:
 23 APPLICATING NUMBER: 02/08/872,855
 24 FILING DATE: 11-JUN-1997
 25 CLASSIFICATION: 514
 26 ATTORNEY/AGENT INFORMATION:
 27 NAME: Atwood, Beth E.
 28 REGISTRATION NUMBER: 65,440
 29 FILING DATE: 02/08/872,855
 30 TELECOMMUNICATION INFORMATION:
 31 TELEPHONE: 617-832-1000
 32 TELEFAX: 617-832-7000
 33 INFORMATION FOR SEQ ID NO: 11:
 34 SEQUENCE CHARACTERISTICS:
 35 LENGTH: 840 amino acids
 36 TYPE: amino acid
 37 STRANDEDNESS:
 38 TOPOLOGY: linear
 39 MOLECULE TYPE: protein
 40 US-08-872-855-11

Query Match 58.4% Score 35; DB 3; Length 830;
 Host Local Similarity 45.5% Prod. No. 93
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 1 BREAKING 11
 1 1 1 1 1
 DB 546 BREAKING 546

RESULT 12
 1 US-08-981-492-6
 2 Sequence 6, Application US/08981492
 3 Patent No. 6262025
 4 GENERAL INFORMATION:
 5 APPLICANT: Ish-Horowicz, David
 6 APPLICANT: Benitque, Camille Mancel Pinto
 7 APPLICANT: Lewis, Julian Hart
 8 APPLICANT: Atavanis-Isakonas, Spyridon
 9 APPLICANT: Gray, Grace
 10 US-08-981-492-6

TITLE OF INVENTION: SUBSTITUTED AND FUSED HETEROCYCLES
 TITLE OF INVENTION: OF VITRIBATE DATA CINES FOR WITH 12 LATER CORRECTION
 NUMBER OF SEQUENCES: 94
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PONTON & Edmund LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036/2713
 COMPUTER READABLE FORM:
 METHOD TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTA, Version 2.0
 CURRENT ATTACHMENT DATA:
 ATTACHMENT NUMBER: 09/08/981, 092
 FILING DATE: 22 May 1997
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Andrew A. Edman M.
 REGISTRATION NUMBER: 42,605
 TELEPHONE: 212 760 9300
 TELEPHONE: 212 760 9300
 TELEFAX: 212-869 0864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 62
 SEQUENCE CHARACTERISTICS:
 LENGTH: 842 amino acids
 TYPE: amino acid
 STRANDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-981-092 6

Query Match: 58.3%, Score 45, Length 842
 Post Local Similarity: 45.5%, Prod. No. 941
 Matches: 52, Mismatches: 27, Indels: 0, Gaps: 0

1 CERAMIN-11
 ID: 548 CHINCHANKV 548

RESULT 13
 US-08-264 544 6
 Sequence 5: Application US/08/264534
 Patent No. 6448464
 CURRENT INVENTION:
 APPLICANT: Attyadris Isakonas, Spytidon et al.
 TITLE OF INVENTION: Human No. 6448464b And Delet, Blasting Isolation
 TITLE OF INVENTION: In Polyphatic Products And Methods Based Thereon
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PONTON & Edmund
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 METHOD TYPE: Floppy disk
 COMPUTER: IBM pc compatible
 OPERATING SYSTEM: pc dos/MS DOS
 SOFTWARE: Pafont to Release #1.0, Version #1.25
 CURRENT ATTACHMENT DATA:
 ATTACHMENT NUMBER: 09/08/264 544
 FILING DATE:
 CLASSIFICATION: 451
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/07/95, 189

FILING DATE: 04 MAY 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: MISTOCK, S. JASITO
 REGISTRATION NUMBER: 19,872
 TELEPHONE: 212 700-0904
 TELEFAX: 212 700-0900
 TELEFAX: 212 869864/9741
 TELEFAX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 63
 SEQUENCE CHARACTERISTICS:
 LENGTH: 843 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08 264 544 6

Query Match: 58.4%, Score 45, Length 843
 Post Local Similarity: 45.5%, Prod. No. 941
 Matches: 52, Mismatches: 27, Indels: 0, Gaps: 0

1 CERAMIN-11
 ID: 548 CHINCHANKV 548

RESULT 14
 US-08-084-590A-2
 Sequence 2: Application US/08/084590A
 Patent No. 5786158
 CURRENT INVENTION:
 APPLICANT: Attyadris Isakonas, S. et al.
 TITLE OF INVENTION: Therapeutic And Diagnostic Methods
 TITLE OF INVENTION: And Compositions Based on No. 5786158b Proteins And
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PONTON & Edmund
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 METHOD TYPE: Floppy disk
 COMPUTER: IBM pc compatible
 OPERATING SYSTEM: pc dos/MS-DOS
 SOFTWARE: Pafont to Release #1.0, Version #1.25
 CURRENT ATTACHMENT DATA:
 ATTACHMENT NUMBER: 09/08/084 590A
 FILING DATE: 25-JUN-1994
 CLASSIFICATION: 451
 ATTORNEY/AGENT INFORMATION:
 NAME: MISTOCK, S. JASITO
 REGISTRATION NUMBER: 19,872
 TELEPHONE: 212 700-0904
 TELEFAX: 212 869864/9741
 TELEFAX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 21
 SEQUENCE CHARACTERISTICS:
 LENGTH: 843 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08 084 590A-2

Query Match: 58.4%, Score 45, Length 843
 Post Local Similarity: 45.5%, Prod. No. 941
 Matches: 52, Mismatches: 27, Indels: 0, Gaps: 0

QY 1 CHAKIMINR1 11
 ID 538 CHAKIMINR1 548

RESULT: 15

US-08-465-500-6

Sequence 6, Application US/08465500

Patent No. 5789195

GENERAL INFORMATION:

APPLICANT: Atavanis-Tsakonas, Spyridon

APPLICANT: Muskavich, Marc A.L.

APPLICANT: Fedos, Richard T.

APPLICANT: Fedos, Richard T.

APPLICANT: Blumel, Christine M.

TITLE OF INVENTION: HUMAN BETA AND DELTA BOUNDING SITES

TITLE OF INVENTION: IN TRANSFERRED PROTEIN AND BETA-1A BOUNDING

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

STREET: 175 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10046-2711

COMPUTER RELEVABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compat (b)

SOFTWARE: Patent Release #1.0, Version #1.10

APPLICATION NUMBER: us-08-465-500

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mistock, S. Los110

REGISTRATION NUMBER: 18,872

REFERENCE/APPET NUMBER: 7126-034

TELECOMMUNICATION INFORMATION:

TELEPHONE: (412) 790-9090

TELEFAX: (412) 869-8844/7741

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 853 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-465-500-6

Query Match: 58.7%; Score 35; 18 L; Length 853

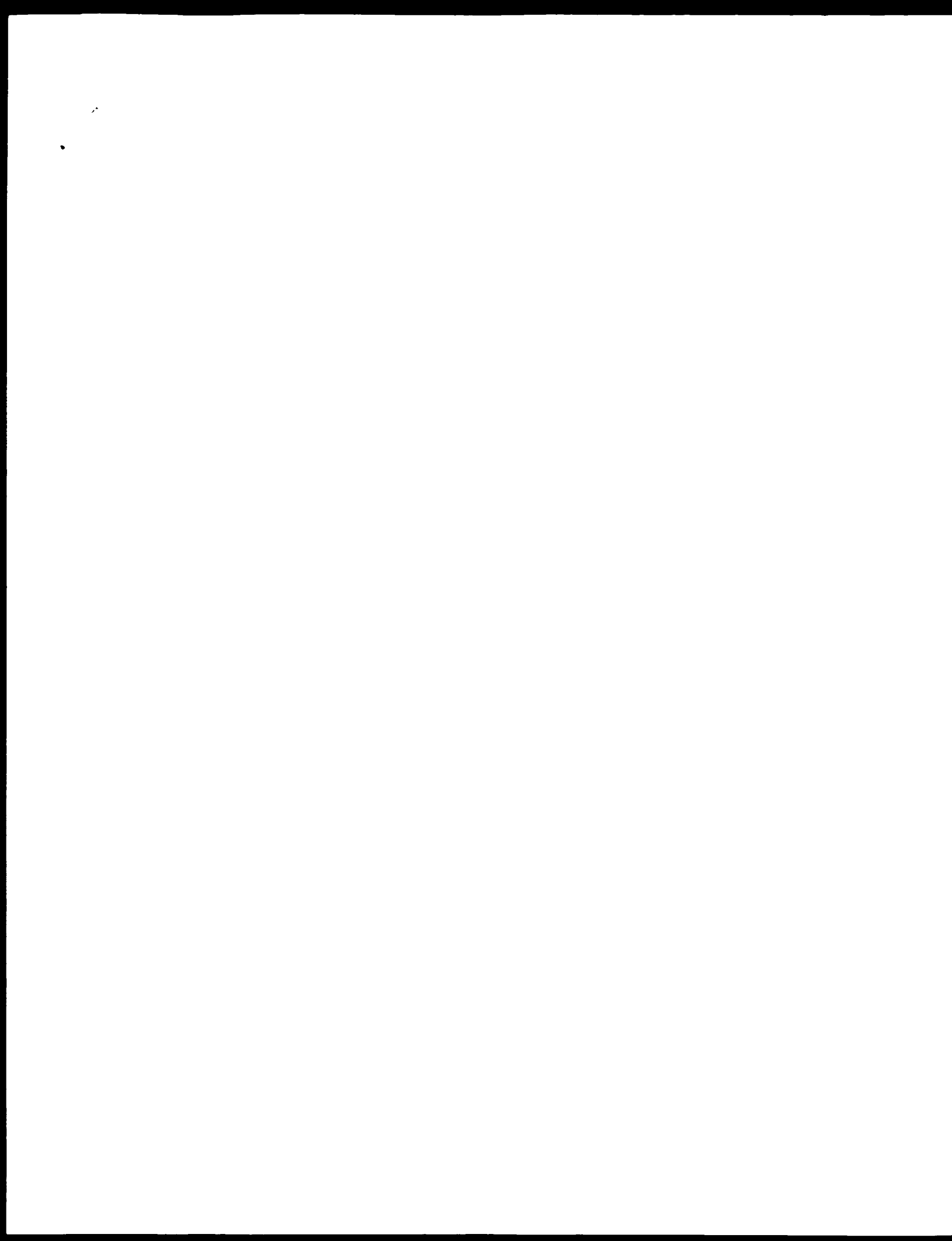
Best Local Similarity: 45.5%; Pred. No. 94;

Matches: 5; Conservative: 2; Mismatches: 4; Indels: 0; Gaps: 0;

QY 1 CHAKIMINR1 11

ID 538 CHAKIMINR1 548

Search completed: July 15, 2002, 14:59:16
 Job time: 144 sec



INDEX

RESEARCH

Figure 1

I-Cell receptor beta chain V-D-J region - mouse (1:4-mutant)

Mosses (Bryophytes)

^c Date: 17-Jul-1992 #sequence_provision 17-Jul-1992 #ext_characte 30-May-1997
^d Accession: P10655

K. J. H. J. A. J.

J. Exp. Med. 174, 115-124, 1991

Attitude: Instructional sequences

A; reference number: P10509; MUID:91277601

Accession: P10655

Aristotle's Poetics

A; status: Translation not shown

A; Molecular type: mRNAs

A. vesiculosus L. - Felt.

At: Export International Services, Inc., 700 West 19th Street, Suite 600, New York, NY 10011-4801
E: Keywords: T-cell receptor

Query Match	28.88	Score 15	DB 2	Length 7
Test Local Similarity	100%			
Pred No	2	8005		

Local Similarity: 100.0%; Pred. No. 2.8e+05

Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 1;

QY 6 A(1)K H

RESULT 15

A21440

variant surface glycoprotein (VSG) - Trypanosoma brucei (fragment)

Species: *Trypanosoma brucei*

(7) Date: 19-Nov-1988 # SOURCE: Division 14-Nov-1988 # EX: Chicago 20-MAY-1988

Accession: A21440

R. Parsons, M.; Nelson, R.G.; Watkins, K.P.; Agabian, N

Cell 48, 309-316, 1984

A:Title: Trypanosome mRNAs share a common 5' spliced leader sequence

Accession number: A90854; MIMD:842827

A: Accession: A21440

A: A (cassion: A21440)

A: Microtubule type: mRNA

A;K:Sidus: 18 · PAR.
A;T:Loss:Potencies: (B;K:0.2]95; MID:q16.2]50; PTD:q16.2]51

Keywords: All-year-round; child

Query Match: 28.8% Score 15: DB 2: Length 8:

Query	Match	Similarity	Prod	NO	DB
Best	100%	1.0	3	80.05	1
Query	Match	28.88%	Score	15	DB 2

Best local Similarity 43.38; Pred. No. 2.8e+05;

УДК 514.51.01

[illegible]

Search completed: July 15, 2002, 14:06:57
Job time: 175 sec

[illegible]

Genotools version 1.5
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0M protein - protein search, using SW model

Run on: July 15, 2002, 14:06:02 ; Search time 12.5 seconds

(without alignments)
50,641 Million cell updates/sec

Title: US-09-719-053a-4

Perfect score: 52

Sequence: 1 MELFLAGRVL 11

Scoring table: HUSUM62

Gapop 10.0 , Gapext 0.5

Search: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 410

Minimum DB seq length: 0

Maximum DB seq length: 11

Post processing: Minimum Match 38

Maximum Match 1000

Listing first 40 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the total score distribution.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match length DB ID Description

1 19 46.5 8 1 CPG1_ENTFA

2 17 42.7 8 1 CAG1_ENTFA

3 17 42.7 9 1 F1H8_EBPFA

4 15 24.8 9 1 F1H8_MACHU

5 15 24.8 9 1 F1H8_EBPFA

6 15 24.8 9 1 F1H8_EBPFA

7 14 24.8 9 1 F1H8_EBPFA

8 14 24.8 9 1 F1H8_EBPFA

9 14 24.8 9 1 F1H8_EBPFA

10 14 24.8 9 1 F1H8_EBPFA

11 14 24.8 9 1 F1H8_EBPFA

12 14 24.8 9 1 F1H8_EBPFA

13 14 24.8 9 1 F1H8_EBPFA

14 14 24.8 9 1 F1H8_EBPFA

15 14 24.8 9 1 F1H8_EBPFA

ALIGNMENTS

34 11 21.2 10 1 CPG1_ENTFA
35 11 21.2 10 1 F1H8_EBPFA
36 11 21.2 10 1 F1H8_MACHU
37 11 21.2 10 1 F1H8_EBPFA
38 11 21.2 10 1 F1H8_EBPFA
39 11 21.2 10 1 F1H8_EBPFA
40 11 21.2 10 1 F1H8_EBPFA
41 11 21.2 10 1 F1H8_EBPFA
42 11 21.2 10 1 F1H8_EBPFA
43 11 21.2 10 1 F1H8_EBPFA
44 11 21.2 10 1 F1H8_EBPFA
45 11 21.2 10 1 F1H8_EBPFA

34 11 21.2 10 1 CPG1_ENTFA
35 11 21.2 10 1 F1H8_EBPFA
36 11 21.2 10 1 F1H8_MACHU
37 11 21.2 10 1 F1H8_EBPFA
38 11 21.2 10 1 F1H8_EBPFA
39 11 21.2 10 1 F1H8_EBPFA
40 11 21.2 10 1 F1H8_EBPFA
41 11 21.2 10 1 F1H8_EBPFA
42 11 21.2 10 1 F1H8_EBPFA
43 11 21.2 10 1 F1H8_EBPFA
44 11 21.2 10 1 F1H8_EBPFA
45 11 21.2 10 1 F1H8_EBPFA

34 11 21.2 10 1 CPG1_ENTFA
35 11 21.2 10 1 F1H8_EBPFA
36 11 21.2 10 1 F1H8_MACHU
37 11 21.2 10 1 F1H8_EBPFA
38 11 21.2 10 1 F1H8_EBPFA
39 11 21.2 10 1 F1H8_EBPFA
40 11 21.2 10 1 F1H8_EBPFA
41 11 21.2 10 1 F1H8_EBPFA
42 11 21.2 10 1 F1H8_EBPFA
43 11 21.2 10 1 F1H8_EBPFA
44 11 21.2 10 1 F1H8_EBPFA
45 11 21.2 10 1 F1H8_EBPFA

34 11 21.2 10 1 CPG1_ENTFA
35 11 21.2 10 1 F1H8_EBPFA
36 11 21.2 10 1 F1H8_MACHU
37 11 21.2 10 1 F1H8_EBPFA
38 11 21.2 10 1 F1H8_EBPFA
39 11 21.2 10 1 F1H8_EBPFA
40 11 21.2 10 1 F1H8_EBPFA
41 11 21.2 10 1 F1H8_EBPFA
42 11 21.2 10 1 F1H8_EBPFA
43 11 21.2 10 1 F1H8_EBPFA
44 11 21.2 10 1 F1H8_EBPFA
45 11 21.2 10 1 F1H8_EBPFA

34 11 21.2 10 1 CPG1_ENTFA
35 11 21.2 10 1 F1H8_EBPFA
36 11 21.2 10 1 F1H8_MACHU
37 11 21.2 10 1 F1H8_EBPFA
38 11 21.2 10 1 F1H8_EBPFA
39 11 21.2 10 1 F1H8_EBPFA
40 11 21.2 10 1 F1H8_EBPFA
41 11 21.2 10 1 F1H8_EBPFA
42 11 21.2 10 1 F1H8_EBPFA
43 11 21.2 10 1 F1H8_EBPFA
44 11 21.2 10 1 F1H8_EBPFA
45 11 21.2 10 1 F1H8_EBPFA

34 11 21.2 10 1 CPG1_ENTFA
35 11 21.2 10 1 F1H8_EBPFA
36 11 21.2 10 1 F1H8_MACHU
37 11 21.2 10 1 F1H8_EBPFA
38 11 21.2 10 1 F1H8_EBPFA
39 11 21.2 10 1 F1H8_EBPFA
40 11 21.2 10 1 F1H8_EBPFA
41 11 21.2 10 1 F1H8_EBPFA
42 11 21.2 10 1 F1H8_EBPFA
43 11 21.2 10 1 F1H8_EBPFA
44 11 21.2 10 1 F1H8_EBPFA
45 11 21.2 10 1 F1H8_EBPFA

34 11 21.2 10 1 CPG1_ENTFA
35 11 21.2 10 1 F1H8_EBPFA
36 11 21.2 10 1 F1H8_MACHU
37 11 21.2 10 1 F1H8_EBPFA
38 11 21.2 10 1 F1H8_EBPFA
39 11 21.2 10 1 F1H8_EBPFA
40 11 21.2 10 1 F1H8_EBPFA
41 11 21.2 10 1 F1H8_EBPFA
42 11 21.2 10 1 F1H8_EBPFA
43 11 21.2 10 1 F1H8_EBPFA
44 11 21.2 10 1 F1H8_EBPFA
45 11 21.2 10 1 F1H8_EBPFA

34 11 21.2 10 1 CPG1_ENTFA
35 11 21.2 10 1 F1H8_EBPFA
36 11 21.2 10 1 F1H8_MACHU
37 11 21.2 10 1 F1H8_EBPFA
38 11 21.2 10 1 F1H8_EBPFA
39 11 21.2 10 1 F1H8_EBPFA
40 11 21.2 10 1 F1H8_EBPFA
41 11 21.2 10 1 F1H8_EBPFA
42 11 21.2 10 1 F1H8_EBPFA
43 11 21.2 10 1 F1H8_EBPFA
44 11 21.2 10 1 F1H8_EBPFA
45 11 21.2 10 1 F1H8_EBPFA

KW Phytoecia 4 AA: 419 MW: 047907287 (SP907 CR064)

QUERY Match 42.7% Score 17: DB 1: Length 4
Best Local Similarity 42.0% Pred. No. 10:05
Matches 4: Conserved 0: Mismatches 1: Indels 0: Gaps 0

QY 4 FLAG 7
1 1 1
DB 4 FLAG 8

RESULT 4
F1 48 ERYIA STANDARD: PRT: 9 AA.

AP F19446
01 NOV 1990 (Ref. 16, created)

DI 01 NOV 1990 (Ref. 16, last sequence update)

DE 01 MAR 2002 (Ref. 41, last annotation update)

DN Fibrinogen beta chain (rodent): Fibrinopeptide B (Fragment).

OS Erythrocytes, Pallas (Rodentium) (Husar).

OC Eukaryota; Metazoa; Chordata; Cladocera; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cerepithecidae;

Genus: Fibrinogen; Erythrocytes.

OX NCBI TaxID 9548;

KN SEQUENCE

RP MEDLINE 85289140; PubMed 9928610;

RA Nakamura S, Takemura K, Takahashi K.

"Fibrinopeptides A and B of Japanese monkey (Macaca fasciata) and

Pallas monkey (Erythrocytes pallas): Their amino acid sequences,

restricted mutations, and a molecular phylogeny for mammals."

RL J. Biochem. 97:1487-1492 (1985).

CC 1. FUNCTION: FIBRINOGEN HAS A PEPTIDE FUNCTION YIELDING 9 NUMBERS THAT

POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN FIBRIN

AGGREGATION.

CC 1. SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS

(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

CC 1. MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS INITIATED BY

THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA

CHAINS, AND THIS EXPOSES THE N-TERMINAL POTENTIAL CATIONIC SITES

RESPONSIBLE FOR THE FORMATION OF THE SOFT GEL.

OK PIR_124180; D24180.

DI InfoPro: IPRO02181; Fibrinogen_C

DI PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.

KW Blood coagulation plasma.

FT PEPTIDE 1 9 FIBRINOPEPTIDE B.

FT NON TER 9 9

SN SEQUENCE 9 AA: 1020 MW: 69167879742018 CR064

QUERY Match 42.7% Score 17: DB 1: Length 4
Best Local Similarity 42.0% Pred. No. 10:05
Matches 4: Conserved 1: Mismatches 0: Indels 0: Gaps 0

QY 2 EFLFAGR 8
1 1 1
DB 3 EFLFAGR 9

RESULT 4
F1 48 MACP3 STANDARD: PRT: 9 AA.

AP F19445

DI 01 NOV 1990 (Ref. 16, created)

DI 01 NOV 1990 (Ref. 16, last sequence update)

DI 01 MAR 2002 (Ref. 41, last annotation update)

DN Fibrinogen beta chain (rodent): Fibrinopeptide B (Fragment).

OS Macaca fasciata fasciata (Japanese macaque).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cerepithecidae;

OC Cerepithecidae; Macaca;

OX NCBI TaxID 9548;

KN SEQUENCE

RP MEDLINE 85289140; PubMed 9928610;

RA Nakamura S, Takemura K, Takahashi K.

"Fibrinopeptides A and B of Japanese monkey (Macaca fasciata) and

Pallas monkey (Erythrocytes pallas): Their amino acid sequences,

restricted mutations, and a molecular phylogeny for mammals."

RL J. Biochem. 97:1487-1492 (1985).

CC 1. FUNCTION: FIBRINOGEN HAS A PEPTIDE FUNCTION YIELDING 9 NUMBERS THAT

POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN FIBRIN

AGGREGATION.

CC 1. SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS

(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

CC 1. MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS INITIATED BY

THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA

CHAINS, AND THIS EXPOSES THE N-TERMINAL POTENTIAL CATIONIC SITES

RESPONSIBLE FOR THE FORMATION OF THE SOFT GEL.

OK PIR_024180; D24180.

DI InfoPro: IPRO02181; Fibrinogen_C

DI PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.

KW Blood coagulation plasma.

FT PEPTIDE 1 9 FIBRINOPEPTIDE B.

FT NON TER 9 9

SN SEQUENCE 9 AA: 1020 MW: 69167879742018 CR064

QUERY Match 28.7% Score 15: DB 1: Length 9
Best Local Similarity 25.0% Pred. No. 10:05
Matches 4: Conserved 0: Mismatches 1: Indels 0: Gaps 0

QY 4 FLAG 7
1 1 1
DB 6 FLAG 9

RA boosdar H., McOolum L.O., Mayer R.L.
 RI purification and characterization of an endo polygalacturonase from
 RI The gut of West Indian sugarcane rootstalk pupa weevil (Callosobruchus
 RI abbreviatus L.) larvae.
 RA Comp. Biochem. Physiol. 118B:661-667(1997).
 CC 1 CATALYTIC ACTIVITY: random hydrolysis of 1,4 glycosidic
 CC galactosiduronic linkages to free the end of the polymer.
 CC 1 INDUCTION: INDUCED BY CLIPROS DGLP.
 CC 1 MISCELLANEOUS: ON THE 2D GEL, THE DETERMINED pI OF THIS PROTEIN IS:
 CC 9.4. ITS MW IS: 44.5 kDa.
 CC 1 SIMILARITY: WEAK TO OTHER POLYGALACTURONASES.
 KM Hydrolyses glycosidases cell walls.
 PT NON-TER
 SV SEQUENCE 9 AA: 1041 MW: 104987042084188 (CR664)

Query Match 26.9% Score 14: DB 1: Length 9:
 Best Local Similarity 40.0% Pred. No. 10000
 Matches 2: Conservative 2: Mismatches 1: Indels 0: Gaps 0:

QY 4 LEAF 8
 DB 4 YVIGR 8

RESULT 10
 ID UAE_HUMAN STANDARD: PRT: 9 AA.
 AC P41941:
 DT 01-JUN-1993 (Rel. 25, created)
 DT 01-JUN-1993 (Rel. 25, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Unknown protein from 2D page of liver tissue (Spot 115) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
 OC Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo:
 OX NCBI_TaxID 9606:
 RN 111
 RP SEQUENCE:
 RC TISSUE: Liver:
 RA MEDLINE 94147969; PubMed 8414870:
 RA Hughes G.D., Fritsch S., Faguet N., Pasquall C., Sanchez J.,
 RA Tissot J.-D., Fritsch A., Appel R.D., Hochstrasser D.F.:
 RA Human liver protein map: update 1993.
 RA Electrophoresis 14:1216-1222(1993).
 CC 1 MISCELLANEOUS: ON THE 2D GEL, THE DETERMINED pI OF THIS PROTEIN IS:
 CC 9.4. ITS MW IS: 44.5 kDa.
 CC 1 PROTEIN IS: 5.5. ITS MW IS: 11 P99.
 SWISS 2DPAGE: P41941: HUMAN.
 FT NON-TER
 SV SEQUENCE 9 AA: 1096 MW: 477848173A272937 (CR664)

Query Match 26.9% Score 14: DB 1: Length 9:
 Best Local Similarity 100.0% Pred. No. 10000
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 LEAF 5
 DB 2 LEAF 4

RESULT 11
 ID UAE_HUMAN STANDARD: PRT: 10 AA.
 AC P42660:
 DT 01-NOV-1995 (Rel. 32, created)
 DT 01-NOV-1995 (Rel. 32, last sequence update)
 DT 10-MAY-2000 (Rel. 49, last annotation update)
 DE Eukaryotic like noncytochrome P-450
 OS MYXILUS cephalis (Blue mussel).
 OC Eukaryota: Metazoa: Mollusca: Bivalvia: Pectiniformia: Mytilidae:
 OX NCBI_TaxID 6550:
 FT NON-TER
 SV SEQUENCE 9 AA: 1041 MW: 104987042084188 (CR664)

RN 111
 RP SEQUENCE:
 RA MEDLINE 93047081; PubMed 1458544:
 RA Walker R.J.:
 RI Nonreactive peptides with an R-peptide or family carboxyl terminal.
 RI Comp. Biochem. Physiol. 122B:213-222(1992).
 CC 1 SIMILARITY: DB 1: ON THE 2D GEL, THE DETERMINED pI OF THIS PROTEIN IS:
 CC 9.4. ITS MW IS: 44.5 kDa.
 KM Non-specific; Amidation.
 PT MOD-RES
 SV SEQUENCE 13 AA: 1180 MW: 12860090174470 (CR664)

Query Match 26.9% Score 14: DB 1: Length 10:
 Best Local Similarity 100.0% Pred. No. 50000
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 LEAF 7
 DB 2 LEAF 4

RESULT 12
 ID EST_RAT STANDARD: PRT: 11 AA.
 AC P56571:
 DT 15-DEC-1998 (Rel. 37, created)
 DT 15-DEC-1998 (Rel. 37, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE EST protein, mitochondrial (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
 OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Murus:
 OX NCBI_TaxID 10116:
 RN 111
 RP SEQUENCE:
 RC STRAIN MISTAK: TISSUE: Heart:
 RA Li X.-F., Plagemer K. P., Seebler C., Smith M.B., K. V., Smith J. L.,
 RA Jonkhoff P.R.:
 RA Submitted (SEP 1996) to the Swiss-Prot data bank.
 CC 1 MISCELLANEOUS: LOCATION: Mitochondrial (fragment).
 CC 1 (Spot P2) IS: 9.9. ITS MW IS: 25 kDa.
 CC 1 SIMILARITY: BELONGS TO THE EST FAMILY.
 KM Mitochondrial.
 FT NON-TER
 SV SEQUENCE 11 AA: 1112 MW: 136227206724072 (CR664)

Query Match 26.9% Score 14: DB 1: Length 11:
 Best Local Similarity 60.0% Pred. No. 57000
 Matches 3: Conservative 1: Mismatches 1: Indels 0: Gaps 0:

QY 3 LEAF 7
 DB 6 EVLSG 10

RESULT 13
 ID UAE_MOUSE STANDARD: PRT: 9 AA.
 AC P99031:
 DT 15-DEC-1998 (Rel. 37, created)
 DT 15-DEC-1998 (Rel. 37, last sequence update)
 DT 15-DEC-1998 (Rel. 37, last annotation update)
 DE Unknown protein from 2D page of liver tissue (Spot 20-001410)
 OS Mus musculus (Mouse).
 OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
 OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus:
 OX NCBI_TaxID 10090:
 RN 111
 RP SEQUENCE:

RC TISSUE: Liver;
 RA Sanchez J, G, Bouge V, Frolicher S, Hughes G, Van J, X,
 RA Hoogland C, Appel R.D., Bliz P.-A., Hochstrasser R.F.,
 RA Coethorne M.;
 RI Submitted (Aug-1998) to the SWISS-PROT data bank;
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED P.I OF THIS UNKNOWN
 CC PROTEIN IS: 5.0, ITS MW IS: 12.5 KDa.
 DR SWISS-2DPAGE: P99041; REUSE;
 FI NON-TER
 SI SEQUENCE 9 AA 1106 MW: E1E842C3240B145A (P99041)

Query Match 25.0%; Score 14; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. Identity
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0

QY 8 FVVL 11
 DB 5 FVVI 8

RESULT 14
 ID TRNK_PIG STANDARD: PRT 10 AA.
 AC P01922;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neurokinin B (NKB) (Neurokinin B).
 GN TAC3 OR NRNR
 OS Sus scrofa (Pig) and
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Phyla: Metazoa; Chordata; Craniata; Vertebrata; Eptostemni;
 OC Mammalia; Mammalia; Carnivora; Canidae; Felidae; Felidae; Felidae;
 OC NCBI:taxid=9623, 8409;
 RN 1;
 RP SEQUENCE;
 RC SPECIES_PIG: TISSUE=Spinal cord;
 RX MEDLINE: 83282812; PubMed: 6576785;
 RA "Protein X, identified as: PIGRA A, Mammal B;
 RI "Neurokinin B: a novel mammalian tachykinin identified in porcine
 RI spinal cord.";
 RL Biochem. Biophys. Res. Commun. 114:533-540(1983).
 RN 12;
 RP SEQUENCE;
 RC SPECIES_R:ridibunda: TISSUE: Brain;
 RX MEDLINE-9204454; PubMed: 168233;
 RA O'Harte F., Burcher E., Jovas S., Smith D.B., Vaudry H., Vaudry J.M.;
 RI "Neurokinin B: a novel NK1 tachykinin receptor agonist isolated with
 RI neurokinin B from the brain of the frog Rana ridibunda.";
 RL J. Neurochem. 57:2086-2091(1991).
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE, INHIBIT,
 CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: A01560; SPPKNS.
 DR InterPro: IPR002040; Tachykinin.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KM Tachykinin, Neuropeptide; Amidation.
 FT MODRES 10 10
 SI SEQUENCE 10 AA: 1211 MW: E1FA7C62799CAAI (P99041)

Query Match 25.0%; Score 14; DB 1; Length 10;
 Best Local Similarity 42.9%; Pred. No. Identity
 Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 1 MELPLAG 7
 DB 2 MDEFFV 8

RESULT 15
 ID TPIS_NICPL STANDARD: PRT 10 AA.
 AC P19118;
 DT 01 NOV 1990 (Rel. 16, Created)
 DT 01 NOV 1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fruiteamut).
 OS Nicotiana glauca (Tobacco) (Leaves of tobacco).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Eudicotyledones; Core eudicot;
 OC Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.
 GN NTL1-taxid=40927;
 RN 11;
 RP SEQUENCE;
 RA Brown J, de Pooze M, Hozier J, van Montagu M, Vanoverbeke J;
 RI "Alterations in the phenotype of plant cells studied by NH2-terminal
 RI amino acid-sequence analysis of proteins electrophoretically
 RI dimensional gel-separated total extracts.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + glyceralone
 CC phosphate.
 CC -1- FAVORABLE FLATS AN IMPOSSIBLE FLATS IN STRAIN RELAXATION FAVORABLE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TIMS, CYTOSOLIC
 CC AND PLASTID.
 CC -1- SIMILARITY: BELONGS TO THE TRI-SEDIMENTAL ISOMERASE FAMILY.
 DR PIR: A27517; A27517.
 DR InterPro: IPR000652; Triosephosphate isomerase.
 DR Pfam: PF00121; TIM; 1.
 DR PROSITE: PS00111; TIM; PARTIAL.
 FM Triosephosphate isomerase; Glucose-6-phosphate; Fatty acid biosynthesis;
 KM Pentose shunt;
 FT NON-TER 10 10
 SI SEQUENCE 10 AA: 1140 MW: 90B9D17862C9C9D1 (P99041)

Query Match 25.0%; Score 14; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. Identity
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0

QY 4 FLAG 7
 DB 5 FVVG 8

Search completed: July 15, 2002, 14:11:24
 Job time: 322 sec



Compucon version 4.5
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OM protein - protein search, using sw model

Run 60: July 15, 2002, 14:05:07 : Search time 39.41 seconds
(without adjustments)
18,249 Million update 5/20/02

Title:	US-09-719-05(A-4
Perfect score:	52
Sequence:	1 MLLFLAGRVL 11

Scoring table: `MIOSUM62`
 Cases: 100 Deleted: 0

Searched: 56222 seqs, 17294929 residues

Total number of hits satisfying chosen parameters: 1416

Minimum PR seq length: 0
Maximum PR seq length: 11

```
Post-processing: Nitro.com March 08
Max mem March 1008
Listing first 45 summaries
```

Database :

```

1:  SP_KENHL:19: *
2:  SP_Archaeo: *
3:  SP_Bacteria:2: *
4:  SP_Fungi: *
5:  SP_Lumini: *
6:  SP_Invertebrate: *
7:  SP_Manual: *
8:  SP_Misc: *
9:  SP_Organot: *
10: SP_Phage: *
11: SP_Plant: *
12: SP_Rotom: *
13: SP_Virus: *
14: SP_WetLable: *
15: SP_WetLassified: *
16: SP_Futrus: *
17: SP_Bacteria: *
18: SP_Archaeo: *

```

pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARY

Result	No.	Score	Major Locality	DB	ID	Description
1	20	48.3	9	7	078225	078225 mus musculus
2	20	48.3	10	6	P82925	078225 mus musculus
3	20	48.3	10	12	Q82625	078225 mus musculus
4	18	44.5	9	7	078226	078226 mus musculus
5	18	44.5	11	10	Q65901	078226 mus musculus
6	17	42.7	8	11	Q90082	078226 mus musculus
7	17	42.7	9	2	Q93550	078226 mus musculus
8	17	42.7	9	11	Q88689	078226 mus musculus
9	17	42.7	9	11	Q82912	078226 mus musculus
10	17	42.7	10	12	Q9P8C3	078226 mus musculus
11	16	40.3	8	2	Q56140	078226 mus musculus
12	16	40.3	8	11	Q9E121	078226 mus musculus
13	16	40.3	10	5	Q55818	078226 mus musculus
14	16	40.3	11	2	Q98R00	078226 mus musculus
15	16	40.3	11	11	Q62207	078226 mus musculus
16	15	28.8	8	4	Q15901	Q15901 homo sapiens

17	28.8	9	2	Q47411	Q47412 mus. musc.
18	28.8	9	1	Q61723	Q61723 mus. musc.
19	28.8	9	12	Q88954	Q88954 vacuolula v
20	28.8	9	13	Q27009	Q27009 gal. lus. gal
21	28.8	10	2	Q47561	Q47561 escherichia
22	28.8	10	5	Q25356	Q25356 locusta mda
23	28.8	11	11	Q60807	Q60807 mus. musc.
24	26.9	8	2	Q9S443	Q9S443 pseudomonas
25	26.9	8	2	Q9S452	Q9S452 pseudomonas
26	26.9	9	9	Q38340	Q38340 lactococcus
27	26.9	10	2	Q9R5N1	Q9R5N1 clostridium
28	26.9	10	2	Q9R5N1	Q9R5N1 clostridium
29	26.9	10	2	Q93145	Q93145 actinobacul
30	26.9	10	6	Q9T2P4	Q9T2P4 ratius sp.
31	26.9	10	11	Q923V2	Q923V2 ratius sp.
32	26.9	10	12	Q93948	Q93948 hepatitis c
33	26.9	10	12	Q9W806	Q9W806 hepatitis c
34	26.9	10	15	Q64980	Q64980 avian myel
35	26.9	11	2	Q9R7J8	Q9R7J8 pseudomonas
36	26.9	11	4	Q9T0J1	Q9T0J1 homo sapien
37	26.9	11	12	Q84074	Q84074 influenza
38	26.9	11	12	Q66200	Q66200 transmissi
39	25.0	8	2	Q32569	Q32569 escherichia
40	25.0	8	4	Q9T4J4	Q9T4J4 homo sapien
41	25.0	8	6	Q9G6M3	Q9G6M3 lactonolignu
42	25.0	9	2	Q9R7E8	Q9R7E8 escherichia
43	25.0	9	4	Q16220	Q16220 homo sapien
44	25.0	9	4	Q9G3V3	Q9G3V3 lactonolignu
45	25.0	9	6	Q9G3V2	Q9G3V2 lactonolignu

APPENDIX

```

RESULT 1
078225
ID 078225 PRIMARY, PR1, 9 AA.
AC 078225
DI 01 NOV-1998 (HEMELREL, OR, Created)
DE 01 NOV-1998 (HEMELREL, OR, Last sequence update)
DT 01-DEC-2001 (HEMELREL, 19, Last annotation update)
DE LYMPHOCYTE ANTIGEN (PROMOT) .
OS Mus musculus (Mouse) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OC NEOL_TaxID=10090;
LN 11
RN SEQUENCE FROM N. A.
RP STRAIN CRO33; TISSUE KIDNEY.
RX MIMMIDR_88084418; PubMed 4692165;
RA Goldberg M., Bonfield O., Schoepfer R., Kasahara M., Mayer W.F.;
RA Finerman F., Klein J.;
RT "Nucleotide sequence analysis of class II genes borne by mouse L
RT chromosomes."
RL Genet. Res. 50:147-146(1987) .
DB EMBL; 13587; AAC02992.1; .
FT NON_COD 1
FT 9
FT 9
NO SUBMITTER 9 AA; 1143 MB; 95661772073633A 078064;

```

Query Match	48.5%	Score 209	DB 7:	Length 92
Query Match	48.5%	Score 209	DB 7:	Length 92

Matches: 4; Conservatively: 2; Mismatches: 4; Indels: 0; Gaps: 0

1 MILLARD, J.

1 I IJKELVPRK 3

PRELIMINARY: 10 AA

[illegible]

Quality	Score	Length
Best local	44.48	17
Similarity	44.48	17
Procl. No.	170004	17
Matches	4	2
Conserved	100	100
Mismatches	0	0
Gap	0	0

RESULT	4			
972625				
11	OR62625	PRELIMINARY:	PRF:	10 AA.
11	OR62625			
11	01 NOV-1996 (11EBMRef. 01, Created)			
11	01 NOV-1996 (11EBMRef. 01, last sequence update)			
11	01 NOV-2001 (11EBMRef. 19, last annotation update)			
11	SMALL ORF			
08	Interfious, burral disease virus (umberto virus).			
07	Virusus; defena virusus; nirevittidus; Aethimivirus.			
0X	NT01_Laxid 109957			
KN	111			
KN	SEQUENCE FROM N.A.			
KX	MEELINE:86,250737; PubMed:30144417			
KX	Hudson P.J., McKern N.M., Power R.E., Azad A.A.:			
K1	"Genomic structure of the large RNA segment of interfious burral disease virus."			
K1	Nucleic Acids Res. 14:5001-5012(1986).			
KN	121			
KN	SEQUENCE FROM N.A.			
KX	MEELINE: 96016880; PubMed: 25524177			
KX	Species H7:			
K1	"Nucleotide sequence of infectious burral disease virus genome segment A of isolates two major open reading frames."			
K1	Nucleic Acids Res. 17:7962-7967(1989).			
KN	131			
KN	SEQUENCE FROM N.A.			
KX	MEELINE: 86250737; PubMed: 30144417			
KX	Buttling H., Spill H., Shaw K., Peters R.W., Papadogiorgaki A., Muller H., Bouillon L.M.H.:			
K1	"A comparison of the sequences of segment A of four different burral disease virus strains and identification of a variable region in V2."			
K1	J. Gen. Virol. 71:1333-1341(1990).			
EMBL	10008697; X000674.1			

DR EMIL: A33255; (AA02)3411; -
 SO SEQUENCE 10 AA; 1376 MW; 5865701617272727 (K6564

Query Match	Score	Score Z	Prob. No.	Length	Top
Best Local Similarity	62.96		1.7e-06		
Matches	57	Conserved	0	Mismatches	47
				Indels	72
				Gaps	0

QY	1	MELP1A000	85
	1	1	1
Db	1	MEL1A000	85

RESULT 4	
078226	
1C 078226	PRELIMINARY; PRT; 9 AA.

[illegible][illegible]

SO SEQUENCE 11 AA: 1208 MW: 602620440997137 bp44

Query Match
Best Local Similarity: 66.7% Score 19; DB 10; Length 11;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPIAG 7
1 1 1 1
DB 1 EXPLOC 6

RESULT 6

ID Q99MH2 PRELIMINARY; PRT; 8 AA.
AC Q99MH2;
DI 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
DI 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
DE CYCLOXYGENASE 2 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Claycomb K. J., Paulsen E., Wu D., Moydant S.N.;
PT "Mouse cycloxygenase 2 (cox-2) gene expression regulated by...";
PI Submitted (FEB-2001) to the EMBL/GenBank/NCBI databases;
DR EMBL: AF344876; AAC27680.1; -;
FT NON_CODING 1
FT NON_CODING 8
SQ SEQUENCE 8 AA: 911 MW: AC087D046C41BA CCK64;

Query Match
Best Local Similarity: 33.7% Score 17; DB 11; Length 9;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LAGR 8
1 1 1 1
DB 5 IAGR 8

RESULT 7

ID Q935G0 PRELIMINARY; PRT; 9 AA.
AC Q935G0;
DI 01-DEC-2001 (TrEMBLrel. 19, created)
DI 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DE HYPOCHELICAL 0.9 KDa PROTEIN (FRAGMENT).
GN HCM2-0001C.
OS Salmonella enterica subsp. enterica serovar typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX VprL_0001_0001;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parbhani U., Joseph C., James F.D., Thomas N.B., Fickard D., Main J.,
RA Churcher G., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies P.M., Dowd L., White N., Barratt J.,
RA Pebody T., Hamlin N., Hargreave A., Hien T.T., Hargreave S., Hargreave G.,
RA Krogh A., Larsen T.S., Leather S., Mould S., O'Garra P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skellern J., Stange K.,
RA Whitehead S., Barrrell B.G.;
PT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar typhi CT18.";

EL NATURE 413:919-922(2001).
DR EMBL: AL513844; CAD09868.1; -;
KW Hypothetical protein; Plasmid.
PW NON_CODING 9
SQ SEQUENCE 9 AA: 901 MW: 2128270721E20D CCK64;

Query Match
Best Local Similarity: 57.1% Score 17; DB 2; Length 9;
Matches 1; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MELIAG 7
1 1 1 1
DB 1 MAVIAG 7

RESULT 8

ID Q88889 PRELIMINARY; PRT; 9 AA.
AC Q88889;
DI 01-NOV-1998 (TrEMBLrel. 08, created)
DI 01-NOV-1998 (TrEMBLrel. 08, last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DE CIRCUTIN CONJUGATING ENZYME UBCM4 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=97057256; PubMed=8901595;
RA Harbers K., Miller U., Grams A., Li F., Tarnitsch F., Franz T.;
RT "Provirus integration into a gene encoding a ubiquitin-conjugating
enzyme results in a placental defect and embryonic lethality";
PI "Proc. Natl. Acad. Sci. U.S.A. 93:12112-12117(1996)."
FT NON_CODING 1
FT NON_CODING 8
SQ SEQUENCE 9 AA: 1063 MW: C90F97341415HDD CCK64;

Query Match
Best Local Similarity: 32.7% Score 17; DB 11; Length 9;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 ASRRV 11
1 1 1 1 1 1
DB 3 ASRRV 8

RESULT 9

ID Q92012 PRELIMINARY; PRT; 9 AA.
AC Q92012;
DI 01-DEC-2001 (TrEMBLrel. 19, created)
DI 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DE SLT12A4 (FRAGMENT).
PW NON_CODING 9

GN ST012A4
 OS Mus musculus (Mouse).
 OT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OT Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 GN NCBI_TaxID:10090.
 RN [1]
 RI SEQUENCE FROM N.A.
 RC STRAIN:12936/SVEVAC, TISSUE:SPLEEN
 RA Eukaryota 8;
 DR EMBL: AF246467; AAL11047.1;
 FT NON_TER
 SO SEQUENCE 9 AA: 1037 MW: 78405041A042CB04 CRG64;

Query Match 42.7%; Score 17; DB 11; Length 9;
 Best Local Similarity 60.0%; Pred. No. 5.6e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 GRV1.11
 DB 1 GRV1.5

RESULT 10
 Q95NCR3 PRELIMINARY: PRT; 10 AA.
 ID Q95NCR3
 AC Q95NCR3
 DT 01-MAY-2000 (TREMBLrel, 13, Created)
 DT 01-MAY-2000 (TREMBLrel, 13, last sequence update)
 DT 01-MAY-2000 (TREMBLrel, 13, last annotation update)
 DE E ANT12FN P2P
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthokepadnavirinae.
 GN NCBI_TaxID:10407;
 RN [1]
 RI SEQUENCE
 RA MEDLINE:92013147; PubMed-1717589;
 RA Takahashi K., Kishimoto S., Ohori K., Yoshizawa H., Machida A.,
 RA Ohnuma H., Tsuda F., Murokawa F., Miyakawa Y., Miyoshi M.;
 RI Molecular heterogeneity of e antigen polypeptides in sera from
 RI carriers of hepatitis B virus *;
 RI J. Immunol. 147:3156-3160(1991).
 SI SEQUENCE 10 AA: 1278 MW: 495ACFEAEK221P07 Q95NCR3

Query Match 32.7%; Score 17; DB 12; Length 10;
 Best Local Similarity 75.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELF.4
 DB 1 MELF.4

RESULT 11
 Q56140 PRELIMINARY: PRT; 8 AA.
 ID Q56140
 AC Q56140
 DT 01-MAY-1996 (TREMBLrel, 01, Created)
 DT 01-MAY-1996 (TREMBLrel, 01, last sequence update)
 DT 01-DEC-2001 (TREMBLrel, 19, last annotation update)
 DE STP6 PROTEIN (FRAGMENT).
 OS Streptococcus thermophilus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 GN NCBI_TaxID:1308;
 RN [1]
 RI SEQUENCE FROM N.A.
 RC STRAIN:ST11;
 RI MEDLINE:95047254; PubMed-7958782;
 RA Constable A., Mollet B.;

RT "Isolation and characterisation of promoter regions from Streptococcus
 RT thermophilus";
 RI FEMS Microbiol. Lett. 122:85-90(1994).
 DE FEMS, 879219; GAA55045.1;
 FT NON_TER
 SO SEQUENCE 8 AA: 846 MW: E086772P5B045B6 CRG64;

Query Match 30.8%; Score 16; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 5.6e+05;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MELF1AG.8
 DB 1 MSLSVPG.8

RESULT 12
 Q9ET21 PRELIMINARY: PRT; 8 AA.
 ID Q9ET21
 AC Q9ET21
 DT 01-MAR-2001 (TREMBLrel, 16, Created)
 DT 01-MAR-2001 (TREMBLrel, 16, last sequence update)
 DT 01-DEC-2001 (TREMBLrel, 19, last annotation update)
 DE PLACENTA GROWTH FACTOR (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 GN NCBI_TaxID:10090;
 RN [1]
 RI SEQUENCE FROM N.A.
 RA MEDLINE:21182783; PubMed-11289150;
 RA Green G.J., Litchfield P., Rugh N.T., Yarovskiy M., Ladereaux K.R.,
 RA Schaffner W., Murphy B.J.;
 RI Placenta growth factor gene expression is induced by hypoxia in
 RI fibroblasts: a central role for metal transcription factor 1 *;
 RI Cancer Res. 61:2696-2704(2001).
 RI EMBL: AF285629; AAC00527.1;
 FT NON_TER
 SI SEQUENCE 8 AA: 992 MW: FFAQC7234622726 CRG64;

Query Match 30.8%; Score 16; DB 11; Length 8;
 Best Local Similarity 75.0%; Pred. No. 5.6e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELF.4
 DB 4 MELF.7

RESULT 13
 Q95NTR8 PRELIMINARY: PRT; 10 AA.
 ID Q95NTR8
 AC Q95NTR8
 DT 01-DEC-2001 (TREMBLrel, 19, Created)
 DT 01-DEC-2001 (TREMBLrel, 19, last sequence update)
 DT 01-DEC-2001 (TREMBLrel, 19, last annotation update)
 DE CYTOCHROME P450 (FRAGMENT).
 GN CYP6D3.
 OS Musca domestica (House fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyoptera; Muscophora;
 OC Muscidae; Muscidae; Musca.
 GN NCBI_TaxID=7370;
 RN [1]
 RI SEQUENCE FROM N.A.
 RC STRAIN-LPR;
 RA Kasai S., Scott J.G.;
 RI "5' flanking sequence of CYP6D3 *";
 RI Submitted (JUN-2000) to the EMBL/GenBank/Trna databases.
 RN [2]
 RI SEQUENCE FROM N.A.

```

RC STRAIN-CS:
RA Kasal S., Scott J.G.:
RT "Chromosome P45C, GP603, 5' flanking sequence."
RL Schemm et al. (May 2000). 11 kb. FMDG 354636.383.1
DB EMBL: AF284258; AAK69543.1; -
DR EMBL: AF284258; AAK69543.1; -
FT NNNLTER
SQ SOURCE 10 AA: 1190 MW: 650409A057272957 CIRC64;

Query Match 30.8%; Score 16; DB 5; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.2e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 MELFL 5
DB 1 MELFL 5

RESULT 14
QRRV0 PRELIMINARY: PRT: 11 AA.
DI 01-MAY-2000 (TREMUR01.13, created)
DI 01-MAY-2000 (TREMUR01.13, last sequence update)
DI 01-DEC-2001 (TREMUR01.19, last annotation update)
DE RES-LVASE (FRAGMENT).
OS Pseudomonas sp. F9.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas
OX NCBI_TaxID=101164;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-P9: TRANSPOSON-TN1404;
PX MEDLINE: 20011227; PMID=10543801;
RA Schobel E.L., Jones A.L.:
RT "Distribution of tetracycline resistance genes and transposons among
RT phytoplano bacteria in Michigan apple orchards."
RL Appl. Environ. Microbiol. 65:4698-4907(1999).
DR EMBL: AF157400; AAI48002.1; -
FT NNNLTER
SQ SOURCE 11 AA: 1407 MW: 100318E258704416 CIRC64;

Query Match 40.8%; Score 16; DB 2; Length 11;
Best Local Similarity 43.3%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 5 LAGRPV 10
DB 1 MCDOKI 6

RESULT 15
Q62207 PRELIMINARY: PRT: 11 AA.
DI 01-NOV-1996 (TREMUR01.01, created)
DI 01-NOV-1996 (TREMUR01.01, last sequence update)
DI 01-DEC-2001 (TREMUR01.19, last annotation update)
DE SCHWANN-MIN (FRAGMENT).
CN NP2 OR NP2.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
EX MEDLINE 95072576; PMID=7961675;
RA Boyan L.P., Nech porok T., Pulst S.-M.:
RT "Alternative transcripts in the mouse neurofibromatosis 1 gene (NF1)
RT gene are conserved and code for schwannin with distinct cytoplasmic

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RT domains."
RL Hum. Mol. Genet. 3:1075-1079(1994).
DR EMBL: L28848; AAK57151.1; -
DE MED. 92:19707-102.
FT NNNLTER
SQ SOURCE 11 AA: 1438 MW: C511A05724140556 CIRC64;

Query Match 30.8%; Score 16; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 7 GRR 9
DB 5 GRR 7

Search completed: July 15, 2002, 14:11:04
Job time: 357 sec

```

10

GenInfo version 4.5
Copyright (c) 1993 2000 CompuLink Ltd.

OR protein - protein search, using SW model

Run on: July 15, 2002, 14:02:52 ; Search time 18.9 seconds
(without alignments)
24,900 hits, 111,077,796 residues

24,900 hits, 111,077,796 residues

Title: us-09-719-053a-4

Perfect score: 52

Sequence: 1 MELFLACPRVL 11

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 747574 seqs, 111077796 residues 14762

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1. A_GenInfo_090902_*
2. A_GenInfo_090902_*
3. A_GenInfo_090902_*
4. A_GenInfo_090902_*
5. A_GenInfo_090902_*
6. A_GenInfo_090902_*
7. A_GenInfo_090902_*
8. A_GenInfo_090902_*
9. A_GenInfo_090902_*
10. A_GenInfo_090902_*
11. A_GenInfo_090902_*
12. A_GenInfo_090902_*
13. A_GenInfo_090902_*
14. A_GenInfo_090902_*
15. A_GenInfo_090902_*
16. A_GenInfo_090902_*
17. A_GenInfo_090902_*
18. A_GenInfo_090902_*
19. A_GenInfo_090902_*
20. A_GenInfo_090902_*
21. A_GenInfo_090902_*
22. A_GenInfo_090902_*

SUMMARIES

Prod. No. is the number of results predicted by chance. The lower
score greater than or equal to the score of the result is not filtered
and is derived by peptide of the total score distributed.

Result No.	Score	Query Match	Length	DB ID	Accession
1	48	92.3	11	21	AAV52292
2	28	52.8	10	22	AAV52292
3	26	50.0	11	14	AAV40875
4	25	48.1	11	14	AAV40875
5	25	48.1	11	14	AAV40875
6	25	48.1	11	14	AAV40875
7	24	46.2	10	21	AAV54244
8	24	46.2	10	22	AAV54244
9	24	46.2	10	22	AAV54244
10	24	46.2	10	22	AAV54244
11	24	46.2	10	22	AAV54244
12	24	46.2	10	22	AAV54244

12	22	42.3	8	22	AAV54244
13	22	42.3	9	20	AAV54244
14	22	42.3	9	21	AAV54244
15	22	42.3	9	21	AAV54244
16	22	42.3	9	21	AAV54244
17	22	42.3	9	22	AAV54244
18	22	42.3	9	22	AAV54244
19	22	42.3	10	19	AAV54244
20	22	42.3	10	20	AAV54244
21	22	42.3	10	20	AAV54244
22	22	42.3	10	21	AAV54244
23	22	42.3	10	21	AAV54244
24	22	42.3	10	21	AAV54244
25	22	42.3	10	21	AAV54244
26	22	42.3	10	22	AAV54244
27	22	42.3	10	22	AAV54244
28	22	42.3	11	14	AAV54244
29	22	42.3	11	16	AAV54244
30	22	42.3	11	22	AAV54244
31	22	40.4	7	18	AAV54244
32	22	40.4	8	14	AAV54244
33	22	40.4	8	14	AAV54244
34	22	40.4	8	14	AAV54244
35	22	40.4	8	14	AAV54244
36	22	40.4	8	19	AAV54244
37	22	40.4	8	19	AAV54244
38	22	40.4	8	22	AAV54244
39	22	40.4	8	22	AAV54244
40	22	40.4	8	22	AAV54244
41	22	40.4	9	11	AAV54244
42	22	40.4	9	16	AAV54244
43	22	40.4	9	16	AAV54244
44	22	40.4	9	16	AAV54244
45	22	40.4	9	20	AAV54244

ALIGNMENTS

RESULT 1

AAV52292 standard: peptide 11 AA.

AAV52292

AAV52292 (11 residues)

AAV52292 (11 residues) peptide 11 AA.

AAV52292 (11 residues) peptide 11 AA.

AAV52292 (11 residues) peptide 11 AA.

AAV52292 (11 residues) peptide 11 AA.

AAV52292 (11 residues) peptide 11 AA.

AAV52292 (11 residues) peptide 11 AA.

AAV52292 (11 residues) peptide 11 AA.

AAV52292 (11 residues) peptide 11 AA.

AAV52292 (11 residues) peptide 11 AA.

AAV52292 (11 residues) peptide 11 AA.

AAV52292 (11 residues) peptide 11 AA.

AAV52292 (11 residues) peptide 11 AA.

AAV52292 (11 residues) peptide 11 AA.

AAV52292 (11 residues) peptide 11 AA.

AAV52292 (11 residues) peptide 11 AA.

AAV52292 (11 residues) peptide 11 AA.

PS Claim 2: Column 17: 19pp: English.
 XX
 CC This sequence represents an antigenic fragment (41) of human acrosomal
 CC sperm protein p34. p34 is a human homologue of the bovine p26b
 CC acrosomal sperm protein which is acquired during epididymal transit.
 CC p26b is known to play a role in gamete interaction as demonstrated by
 CC the ability of anti-p26b antibodies to inhibit sperm/zona pellucida
 CC binding in vivo and in vitro. It exhibits immunoreactive properties
 CC when used to actively immunize male hamsters. Similarly, p34 has
 CC potential for use in immunovaccine vaccine in humans. p34
 CC is specifically expressed in the epididymis, which supports its
 CC potential as an immunovaccine target. An immunovaccine
 CC vaccine may comprise antigenic fragments of p34 (e.g., this sequence, or
 CC AA952293), and an immune response should be generated against the p34
 CC fragments when administered to men. As the blood-testis barrier is not
 CC present in the epididymis, the antibodies should reach the spermatozoa
 CC and neutralise the fertilising ability of the spermatozoa, thus
 CC conferring an immunovaccine protective protection.

XX Sequence 11 AA:

Query Match 92.8% Score 48: 18 27: Length 11
 Best Local Similarity 100.0% Prod. No. 0.0032
 Matches 10: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 1 MEPLAGRRV 10
 ID 1 MEPLAGRRV 10

RESULT 2

AA97416
 ID AA97416 standard; Peptide: 10 AA.

XX AA97416:

XX 18-SEP-2001 (first entry)

XX Human complementary peptide; SEQ ID NO: 4010.

XX Human complementary peptide; drug discovery; drug design.

XX Homo sapiens.

XX W020014277 AL.

XX 14 JUN 2001.

XX 13 DEC 2000: 2000WO-G004776.

XX 13 DEC 1999: 99GB 0029404.

XX (PCT) PROTEOM LTD.

XX Roberts CM, Hoel DK

XX WPI: 2501-408419743.

XX A set of peptide ligands consisting of specific complementary peptides
 XX for proteins encoded by genes of the human genome, useful in an assay
 XX for screening and identifying of one or more novel peptides which are
 XX drug candidates or products

XX Example 4: Page 561: 64pp: English.

XX The invention relates to a set of complementary peptide ligands
 XX generated from the human genome. The complementary peptides
 XX interact with their relevant target proteins encoded in the human
 XX genome. They can be used as reagents in drug discovery and as lead
 XX ligands to facilitate drug design and development. The present
 XX sequence is a complementary peptide provided in the specified form.

SU Sequence 10 AA:

Query Match 59.8% Score 29: 18 22: Length 10
 Best Local Similarity 86.7% Prod. No. 962
 Matches 5: Conservative 4: Mismatches 1: Indels 0: Gaps 0

QY 3 LEPLAGRRV 11
 ID 3 LEPLAGRRV 11

XX AAR40875:

XX AAR40875 standard; Protein: 11 AA.

XX 20 MAR-1994 (first entry)

XX SSP for Flavonoid 3',5'-hydroxylase gene.

XX 16-SEP-1993.

XX W09318155-A.

XX Potunia hybrid.

XX W09318155-A.

XX 20-NOV-1992: 92WO JP01520.

XX 02-MAR-1992: 92JP 0044963.

XX (EYEW) EY-6A BAKO 606V-09 LTD.

XX Kikuchi Y, Kiyokawa S, Ohnishi M, Yoshida Y, Shimada K

XX Shimada Y

XX WPI: 1993-303469/38.

XX N-PSDB: AA047876.

XX Gene coding for flavonoid 3',5'-hydroxylase of Potunia petals

XX used to transform plants (e.g. Potunia, rose or tobacco) to give

XX bluer flower colour and altered pigment pattern

XX Claim 11: Page 57: 84pp: Japanese.

XX Insertion of the sequence (AA047876-42) into plants such as rose,
 XX petunia, tobacco, and carnation, using a suitable vector such as
 XX agro bacterium, give transformed plants which express the gene,
 XX resulting in petals with a bluer colour than normal, and/or

XX pigment pattern patterns which do not occur naturally. The sequence
 XX were amplified using primers (AA047843-70). Related single specific
 XX primers using a gene sequence coding for the haem-binding region of
 XX cytochrome P450 are shown in (AA047871-947963).

XX Sequence 11 AA:

Query Match 50.0% Score 26: 18 14: Length 11
 Best Local Similarity 86.7% Prod. No. 962
 Matches 6: Conservative 0: Mismatches 1: Indels 0: Gaps 0

QY 4 FLACRRV 10
 ID 4 FLACRRV 10

RESULT 4
 AAR40871

ID AAR40871 standard; Protein: 11 AA.
 XX
 AC AAR40871:
 XX
 DI 28-MAR-1994 (first entry)
 XX
 DE SSP for flavonoid 3',5'-hydroxylase gene product.
 XX
 KW Flavonoid 3',5'-hydroxylase; transformation; plant; petal; rose
 KM tobacco; pigment alteration; blue; SSP; single specific primer;
 KU PCR; polymerase chain reaction; amplification; expression;
 XX
 OS Petunia hybrida.
 XX
 PN W09318155-A.
 XX
 DI 16-SEP-1994.
 XX
 DE 20-NOV-1992: 92WO-CP01520.
 XX
 PR 02-MAR-1992: 92JP-0044963.
 XX
 PA (KYW) KYWA HAREO KORYO CO LTD
 XX
 PI Kikuchi Y, Kikuchi S, Ohgushi M, Chikada Y, Shimada Y,
 PI Shimada Y:
 XX
 DI WPI: 1993-303469/78
 XX
 DE N-PSDB: AAC47872
 XX
 PI Gene coding for flavonoid 3',5'-hydroxylase of petunia petals -
 PI used to transform plants e.g. petunia, rose or tobacco to give
 PI blue flower colour and altered pigment pattern
 XX
 PS Claim 11: Page 56; 82pp; Japanese.
 XX
 DI Insectin of the sequences (AAC47843-42) into plasmids such as pSP6,
 XX petunia, tobacco and carnation, using a suitable vector such as
 XX an expression vector or expression plasmid which expresses the gene,
 XX resulting in petals with a blue colour than normal, and/or
 XX pigment alteration patterns which do not occur naturally. The sequences
 XX were amplified using primers (AAC47843-70). Related single specific
 XX primers using a gene sequence coding for the haem binding region of
 XX cytochrome P450 are shown in (AAC47871-047903).
 XX
 SU Sequence 11 AA:
 XX
 Query Match 48.1% Score 25; DI 14; Length 11;
 Best Local Similarity 71.4% Fred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 1; Gaps 0;
 QY 4 FLAGRV 10
 DI 11111:
 DI 2 FLAGRV 8
 XX
 DE SSP for flavonoid 3',5'-hydroxylase gene product.
 XX
 KW Flavonoid 3',5'-hydroxylase; transformation; plants; petunia; rose;
 KM tobacco; pigment alteration; blue; SSP; single specific primer;
 KU PCR; polymerase chain reaction; amplification; expression;
 XX
 OS Petunia hybrida.
 XX
 PN W09318155-A.
 XX
 DI 16-SEP-1994.
 XX
 DE 20-NOV-1992: 92WO-CP01520.
 XX
 PR 02-MAR-1992: 92JP-0044963.
 XX
 PA (KYW) KYWA HAREO KORYO CO LTD.
 XX
 PI Kikuchi Y, Kikuchi S, Ohgushi M, Chikada Y, Shimada Y,
 PI Shimada Y:
 XX
 DI WPI: 1993-303469/78.
 XX
 DE N-PSDB: AAC47873.
 XX
 PI Gene coding for flavonoid 3',5'-hydroxylase of petunia petals -
 PI used to transform plants e.g. petunia, rose or tobacco to give
 PI blue flower colour and altered pigment pattern
 XX
 PS Claim 11: Page 56; 82pp; Japanese.
 XX
 DI Insectin of the sequences (AAC47843-42) into plasmids such as pSP6,
 XX petunia, tobacco and carnation, using a suitable vector such as
 XX an expression vector or expression plasmid which expresses the gene,
 XX resulting in petals with a blue colour than normal, and/or
 XX pigment alteration patterns which do not occur naturally. The sequences
 XX were amplified using primers (AAC47843-70). Related single specific
 XX primers using a gene sequence coding for the haem binding region of
 XX cytochrome P450 are shown in (AAC47871-047903).
 XX
 SU Sequence 11 AA:
 XX
 Query Match 48.1% Score 25; DI 14; Length 11;
 Best Local Similarity 71.4% Fred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 1; Gaps 0;
 QY 4 FLAGRV 10
 DI 11111:
 DI 2 FLAGRV 8
 XX
 DE SSP for flavonoid 3',5'-hydroxylase gene product.
 XX
 KW Flavonoid 3',5'-hydroxylase; transformation; plants; petunia; rose;
 KM tobacco; pigment alteration; blue; SSP; single specific primer;
 KU PCR; polymerase chain reaction; amplification; expression;
 XX
 OS Petunia hybrida.
 XX
 PN W09318155-A.
 XX
 DI 16-SEP-1994.
 XX
 DE 20-NOV-1992: 92WO-CP01520.
 XX
 PR 02-MAR-1992: 92JP-0044963.
 XX
 PA (KYW) KYWA HAREO KORYO CO LTD.
 XX
 PI Kikuchi Y, Kikuchi S, Ohgushi M, Chikada Y, Shimada Y,
 PI Shimada Y:
 XX
 DI WPI: 1993-303469/78.
 XX

PN W09318155-A.
 XX
 DI 16-SEP-1994.
 XX
 DE 20-NOV-1992: 92WO-CP01520.
 XX
 PR 02-MAR-1992: 92JP-0044963.
 XX
 PA (KYW) KYWA HAREO KORYO CO LTD.
 XX
 PI Kikuchi Y, Kikuchi S, Ohgushi M, Chikada Y, Shimada Y,
 PI Shimada Y:
 XX
 DI WPI: 1993-303469/78.
 XX
 DE N-PSDB: AAC47873.
 XX
 PI Gene coding for flavonoid 3',5'-hydroxylase of petunia petals -
 PI used to transform plants e.g. petunia, rose or tobacco to give
 PI blue flower colour and altered pigment pattern
 XX
 PS Claim 11: Page 56; 82pp; Japanese.
 XX
 DI Insectin of the sequences (AAC47843-42) into plasmids such as pSP6,
 XX petunia, tobacco and carnation, using a suitable vector such as
 XX an expression vector or expression plasmid which expresses the gene,
 XX resulting in petals with a blue colour than normal, and/or
 XX pigment alteration patterns which do not occur naturally. The sequences
 XX were amplified using primers (AAC47843-70). Related single specific
 XX primers using a gene sequence coding for the haem binding region of
 XX cytochrome P450 are shown in (AAC47871-047903).
 XX
 SU Sequence 11 AA:
 XX
 Query Match 48.1% Score 25; DI 14; Length 11;
 Best Local Similarity 71.4% Fred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 1; Gaps 0;
 QY 4 FLAGRV 10
 DI 11111:
 DI 2 FLAGRV 8
 XX
 DE SSP for flavonoid 3',5'-hydroxylase gene product.
 XX
 KW Flavonoid 3',5'-hydroxylase; transformation; plants; petunia; rose;
 KM tobacco; pigment alteration; blue; SSP; single specific primer;
 KU PCR; polymerase chain reaction; amplification; expression;
 XX
 OS Petunia hybrida.
 XX
 PN W09318155-A.
 XX
 DI 16-SEP-1994.
 XX
 DE 20-NOV-1992: 92WO-CP01520.
 XX
 PR 02-MAR-1992: 92JP-0044963.
 XX
 PA (KYW) KYWA HAREO KORYO CO LTD.
 XX
 PI Kikuchi Y, Kikuchi S, Ohgushi M, Chikada Y, Shimada Y,
 PI Shimada Y:
 XX
 DI WPI: 1993-303469/78.
 XX

PI autoimmune diseases.

XX
XX disclosure Page 66: 12pp: English.

XX
XX AAV7266-974 are potential peptide binders of HLA A*01 and the binding motifs disclosed in the invention, these peptides were screened for further motifs, only peptides with binding affinity of at least 1X (binding affinity is expressed as an IC50 value) at concentration of the standard peptide (AAV71994) in assays. This peptide from MATHINC) has a binding motif of 9-2200 (new peptide of the invention) and binds to the cytotoxic T lymphocytes which can react with tumor cells. The 9 can be used for the treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma, etc.

XX
XX Sequence 9 AA:

Query Match 42.3% Score 22 DB 17 Length 7
Host Local Similarity 62.5% Pred No. 6.4e+05
Matches 5: Conservative 1: Mismatches 2: Indels 0: Gaps 0:

QY 3 LFLASRRV 10
DB 2 mlwpprv 9
211111

RESULT 14
AAV47278
ID AAV47278 standard, Peptide: 9 AA.

XX
XX AAV47278:

XX
XX 01-DEC-1999 (first entry)

XX
XX Immunogenic peptide having a human leukocyte antigen binding motif #1889.

XX
XX Human leukocyte antigen binding immunization epitope from HBT, HLA immune response T cell activation, major histocompatibility complex, 1/100000 T lymphocyte, 010, tumor reject and viral infection, cancer, prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, vaccine, immunisation.

XX
XX Synthetic.

XX
XX Homo sapiens.

XX
XX WO945954-A1.

XX
XX 16-SEP-1994.

XX
XX 13-MAR-1998: 96WO-0505039.

XX
XX 13-MAR-1998: 96WO-0505049.

XX
XX (EPIM-) EPIMTNE INC.

XX
XX Sarte A Kye et al, Sidney H, Collins F, Cheng W, Scott et al, 1999, WPI: 1999-551119/46.

XX
XX New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases.

XX
XX Claim 1: Page 101: 150pp: English.

XX
XX AAV5339 to AAV5214 represent specifically related immunogenic peptides having a human major histocompatibility complex (MHC) Class I (class I known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (class I HLA A subtypes: HLA-A*01, A*02 or A*03) or HLA B or C2 and induce a cytotoxic T cell response against the antigen from which the peptide is derived.

XX
XX cytotoxic T lymphocytes (CTLs) which destroy antigen bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign protein, as in the

XX are particularly important in tumor rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancer, in particular, colorectal cancer, prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.

XX
XX They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response by conducting a cytotoxic T cell with the peptide e.g. to fight CTLs or to fight infection. In a further embodiment, the peptides and polypeptides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.

XX
XX Sequence 9 AA:

Query Match 42.3% Score 22 DB 20 Length 9
Host Local Similarity 62.5% Pred No. 6.4e+05
Matches 5: Conservative 1: Mismatches 2: Indels 0: Gaps 0:

QY 4 LFLASRRV 10
DB 2 mlwpprv 9
211111

RESULT 15
AAV94561
ID AAV94561 standard, Peptide: 9 AA.

XX
XX AAV94561:

XX
XX 22-AUG-2000 (first entry)

XX
XX Human 514 tumor associated antigen gene #8.

XX
XX Human TAA, tumor associated antigen, anti-tumor, cytostatic, immunomodulatory, vaccine, carcinoma, colorectal cancer, gastric cancer.

XX
XX Homo sapiens.

XX
XX W0200029428-A2.

XX
XX 25-MAY-2000.

XX
XX 18-NOV-1999: 99WO-GB03859.

XX
XX 18-NOV-1999: 98GB-0025303.

XX
XX 27 JAN-1999: 99GB-0001739.

XX
XX 30-JUL-1999: 99GB-0017995.

XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX
XX Carroll MW, Myers KA:

XX
XX WPI: 2000-207335/73.

XX
XX Tumor associated antigen, 514, capable of eliciting cytotoxic T lymphocyte response useful in vaccinating against and in treating tumors.

XX
XX Example 10: Page 48: 79pp: English.

XX
XX The present sequence is one of a number of peptide fragments derived from 514 which are able to function as 514-specific and HLA-A*01 determinants. They are able to bind HLA A*01 and to induce CTL response against wild type 514. 514 is a tumor associated antigen (TAA) which is widely expressed in carcinomas but has a highly restricted expression pattern in normal adult tissues. It appears to be strongly correlated to metastasis in colorectal and gastric cancer. 514 antigen may therefore be useful in tumor diagnosis, targeting and immunotherapy. Mice in which tumors had been induced were inoculated with a virus expression vector containing the present sequence, the 514 antigen

was shown to be effective at eliciting an immunological response to anti-tuberc
response, both the nucleic acid encoding the antigen and the antigen
itself can be used to elicit an immune response, preferably of Th1 or an
anti-body response in a subject.

XX Sequence 9 AA)

Query Match 42.4% Score 22 DB 21 Length 9
Best Local Similarity 51.0% Prod. No. 6,44,057
Matches 4: Conservative 2: Mismatches 2: Indels 0: Gaps 0

QY 4 LFLAVRRV 10
111133
10 2 1114001 9

Search completed: July 15, 2002, 14:05:59
Job time: 1hr 50m

GenCore version 4.5
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OK protein: protein search, using SW Model

Run on: July 15, 2002, 14:06:57 : Search time 25.00 seconds
(without alignment)

42,245 Matches on 11 updates/26

Hit(s): US-09-719-053a-5

Perfect score: 60

Sequence: 1 CHKA1MIMN1.11

Scoring table: BLAST/MSD/2

Gapop 10.0, Gapext 0.5

Searched: 28438 seqs, 9609334 residues 1x25

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: PIR71:*

2: PIR71:*

3: PIR71:*

4: PIR71:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query	Match Length	ID	Description
1	25	41.7	11	A14454	6-phosphofructokin
2	18	39.0	10	S65387	cytochrome oxidase
3	17	28.3	7	S08606	cytochrome oxidase
4	17	28.3	11	A61483	cytochrome oxidase
5	16	26.7	8	S53008	cytochrome oxidase
6	16	26.7	10	S53282	cytochrome oxidase
7	16	26.7	11	A11136	cytochrome oxidase
8	15	25.0	7	S38916	cytochrome oxidase
9	15	25.0	9	S54779	cytochrome oxidase
10	15	25.0	10	S39798	cytochrome oxidase
11	15	25.0	10	PH8807	cytochrome oxidase
12	14	23.2	7	S13373	cytochrome oxidase
13	14	23.2	9	S55696	cytochrome oxidase
14	14	23.2	9	T31612	cytochrome oxidase
15	14	23.2	9	PH0935	cytochrome oxidase
16	14	23.2	10	S60234	cytochrome oxidase
17	14	23.2	10	S23307	cytochrome oxidase
18	14	23.2	10	S23186	cytochrome oxidase
19	14	23.2	10	S27129	cytochrome oxidase
20	14	23.2	10	A44871	cytochrome oxidase
21	14	23.2	10	S60753	cytochrome oxidase
22	14	23.2	10	S74147	cytochrome oxidase
23	14	23.2	10	S54823	cytochrome oxidase
24	14	23.2	10	S54922	cytochrome oxidase
25	14	23.2	11	S33519	cytochrome oxidase
26	13	21.7	4	GKHU	cytochrome oxidase
27	13	21.7	4	A22565	cytochrome oxidase
28	13	21.7	5	A40702	cytochrome oxidase
29	13	21.7	5	P22565	cytochrome oxidase

30	13	21.7	6	JN0861	peptidyl dipeptidase
31	13	21.7	2	S71667	aspartate transaminase
32	13	21.7	7	A11484	aspartate transaminase
33	13	21.7	9	S19429	aspartate transaminase
34	13	21.7	10	S15116	aspartate transaminase
35	13	21.7	10	S15116	aspartate transaminase
36	13	21.7	10	S15116	aspartate transaminase
37	13	21.7	10	S15116	aspartate transaminase
38	13	21.7	10	S15116	aspartate transaminase
39	13	21.7	10	S15116	aspartate transaminase
40	13	21.7	10	S15116	aspartate transaminase
41	13	21.7	10	S15116	aspartate transaminase
42	13	21.7	10	S15116	aspartate transaminase
43	13	21.7	10	S15116	aspartate transaminase
44	13	21.7	10	S15116	aspartate transaminase
45	13	21.7	10	S15116	aspartate transaminase

ALIGNMENTS

RESULT 1
A14454
6-phosphofructokinase (EC 2.7.1.11) sheep (fragment)
C:Species: Ovis montanus aries, Ovis ammon aries (domestic sheep)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 28-Apr-1993
C:Accession: A14454
R:Portage, A.M.; Midwinter, G.G.; Moore, C.H.
Biochem. Soc. Trans. 7: 721-723, 1979
A:Title: The 8 terminal amino acid sequence of sheep heart phosphofructokinase.
A:Reference number: A14454; M01080004524
A:Accession: A14454
A:Molecule type: protein
A:Keywords: 1-11 SPOR
C:Keywords: glycolysis; phosphotransferase

Query Match 41.7% Score 25 DB 27 Length 11
Post local similarity 66.7% Pred. No. 1,80922
Mismatch 41 Conserved 21 Mismatch 01 Indels 01 Gaps 01

QY 2 HKATL 7
DB 6 HKATL 11

RESULT 2
S65387
cytochrome oxidase (EC 1.9.3.1) chain VII b, cardiac - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Feb-1988 #sequence_revision 20-Feb-1988 #text_change 16-Jul-1999
C:Accession: S65387; S65386
R:Schaefer, H.; Neuk, H.; Hahnke, W.; Brandt, H.; von Jadow, G.
Eur. J. Biochem. 235: 241-241, 1995

A:Title: Cytochrome c oxidase in developing rat heart: Enzymic properties and amino acid
A:Keywords: 1-10 S652
C:Keywords: cardiac muscle; heart; oxidoreductase

A:Accession: S65387
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 (S65)
A:Accession: S65386
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 (S65)
C:Keywords: cardiac muscle; heart; oxidoreductase

Query Match 29.0% Score 19 DB 27 Length 10
Post local similarity 60.0% Pred. No. 3,70043
Mismatch 47 Conserved 11 Mismatch 11 Indels 01 Gaps 01

QY 2 HKATL 6
DB 11

A:Reference number: S48516; MUID:94002261
 A:Accession: S48516
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <NR>

Query Match 25.0%; Score 15; PB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHKA 4
 DB 1 CORA 4

RESULT 9
 154379

Gene NF2 protein - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 01-Nov-1995 #sequence_revision 03 Nov 1996 #text_change 21 Jul 2000
 C:Accession: 154379
 E:Alaiz, E.; Kouchi, F.; Nakamura, Y.
 Hum. Mol. Genet. 3: 937-939, 1994
 A:Title: Characterization of the translocation breakpoint on chromosome 22p12.2 in a p53
 A:Reference number: 154379; MUID:95048750
 A:Accession: 154379
 A>Status: preliminary; translated from cDNA/EMBL/DBM
 A:Molecule type: DNA
 A:Residues: 1-9 <RES>
 A:Cross-references: GR:S57841; NID:q861532; PIRN:AD14190.1; PIR:q4261890
 C:Comment:
 A:Gene: GDB:NF2
 A:Cross-references: GDB:129732; CIRM:101909
 A:Map position: 22q12.2-22q12.2

Query Match 25.0%; Score 15; PB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LNR 10
 DB 1 LNR 3

RESULT 10
 839308
 A:Title: reductase (EC 1.4.99.-) sulphydryl protein of beta chain - chloridium sticklandii
 C:Species: Chloridium sticklandii
 C:Date: 19-Jun-1992 #sequence_revision 10-Jan-1992 #text_change 15-Aug-1997
 C:Accession: 839308
 E:Stadman, T.C.; Davis, J.N.
 J. Biol. Chem. 266: 22147-22153, 1991
 A:Title: Amino acid reductase protein of Chloridium sticklandii: properties and characterization of its role in the
 A:Abstract: Amino acid reductase protein of Chloridium sticklandii
 A:Accession: 839308
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <SIA>
 C:Function:
 A:Description: Amino acid reductase complex catalyzes the reduction bromination of amino
 C:Keywords: Amino acid reductase

Query Match 25.0%; Score 15; PB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 LNR 11
 DB 4 LNR 6

RESULT 11

PH0807

1-cell receptor alpha chain (34) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PH0807

E:Casanova, J.L.; Romero, P.; Wilmar, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174: 1371-1383, 1991

A:Title: 1-cell receptor genes in a series of class I major histocompatibility complex

allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078646

A:Accession: PH0807

A:Molecule type: mRNA

A:Residues: 1-10 <RES>

A:Cross-references: EMBL:X60916

A:Experimental source: T lymphocyte

C:Keywords: 1-cell receptor

Query Match 25.0%; Score 15; PB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NRI 11
 DB 5 NRI 7

RESULT 12

S1333

alpha/beta gliadin - wheat (fragment)

C:Species: Triticum aestivum (common wheat)

C:Date: 19-Mar-1992 #sequence_revision 30-Jan-1998 #text_change 10-Jan-1998

C:Accession: S1333

E:Arrau, A.P.; An, G.; Okita, T.W.

Mol. Gen. Genet. 225: 65-71, 1991

A:Title: Structural and functional analysis of promoter from gliadin, an endosperm-sp

A:Reference number: S1333; MUID:91159436

A:Accession: S1333

A:Molecule type: DNA

A:Residues: 1-9 <ARY>

Query Match 23.2%; Score 14; PB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KIML 8
 DB 2 KIML 5

RESULT 13

S55696

Phosphoenolpyruvate carboxylase 1 (phosphoenolpyruvate

C:Species: Trypanosoma brucei

C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999

C:Accession: S55696

E:Rihm, M.; Koehler, P.

Biochim. Biophys. Acta 1249: 15-22, 1995

A:Title: Purification and characterization of phosphoenolpyruvate carboxylase from

A:Reference number: S55696; MUID:95284106

A:Accession: S55696

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 <HUN>

Query Match 23.4%; Score 14; PB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 BKAK 6
1 1
DB 5 BKAK 9

RESULT 14

141612

lyso bacterial protein Y50BBA.h - Caenorhabditis elegans

Accession: caenorhabditis_oligos

Cloned: 29 Oct 1999 #sequence_translation 29 Oct 1999 #prot_change 29 Oct 1999

Accession: 141612

Resubmitted:

submitted to the EMBL Data Library: September 1999

Accession number: Z21047

Accession: 141612

Accession: preliminary: translated from ORF/EMBL/GenBank

Accession type: DNA

Accession: 1-9-0001

Accession: EMBL:AL117209; NID:01549770; EID:0704857511; EST:Y50BBA.h

Accession: experimental source: clone Y50BBA

Accession: 1-9-0001

Accession: CEST:Y50BBA.h

Query Match 24.4% Score 14; DB 2; Length 92
Best Local Similarity 50.0% Prod. No. 2,86,065
No. Obs. 2; Conservation 1; Mismatches 3; Indels 0; Gaps 0

QY 2 BKAK 6
1 1
DB 5 BKAK 9

RESULT 15

PH0945

T cell receptor beta chain V-D-J region (clone 6) - rat (transmembr)

Accession: Rattus norvegicus (Norway rat)

Cloned: 09 Oct 1992 #sequence_translation 09 Oct 1992 #prot_change 30 May 1997

Accession: PH0945

Rebold, D.P.; O'Neil, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

Accession: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic

Accession number: PH0945; MIMD:92078857

Accession: PH0945

Accession type: mRNA

Accession: 1-9-0001

Accession: experimental source: complementary cDNA from immunized lymph node

Accession: 1-9-0001

Accession: CEST:Y50BBA.h

Query Match 24.4% Score 14; DB 2; Length 92
Best Local Similarity 50.0% Prod. No. 2,86,065
Matches 2; Conservation 1; Mismatches 3; Indels 0; Gaps 0

QY 1 BKAK 6
1 1
DB 1 CASSET 6

Search completed: July 15, 2002, 14:06:58
Job time: 176 sec


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RP MEDLINE 9417969; PubMed 9417970;
RX Yoshino K, Ito T, Kato T, Shimidzu Y, Suzuki N.
R1 Identification of the amino acid sequence of an intramolecular
R2 disulfide linkage connecting sperm actin and tropomyosin
R3 spectrometry.
R4 FEBS Lett. 294:179-182(1991).
R5 1. FUNCTION: CAUSE INHIBITION OF Sperm PRETREATION AND MOTILITY
R6 THROUGH THE CAUSE OF ALKALINIZING AND CONDENSATION OF
R7 GAMP, FORMING PLASMA MEMBRANE IN SPERM CELLS AND TRANSFER
R8 ACTIVITY AND CONDENSATION TO VACUOLIN AND MEMBRANE FORM
R9 GUANYLATE CYCLASE.
DR PIR: S19329; S19329.
FT DISUFLD 4
SQ SEQUENCE 9 AA: 1010 MW: 64609.087072300 CPG64;

Query Match 21.7% Score 14; DB 1; Length 10;
Best Local Similarity 45.0%; Prot. No. 7.6e+05;
Matches 2; Conserved 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CHIRAK 5
ID 1 1
ID 3 CHIRAK 7

RESULT 12
UPAS_HUMAN
ID UPAS_HUMAN STANDARD; PRT; 10 AA.
AC P00911;
D1 01-APR-1994 (rel. 25, created)
D2 01-APR-1994 (rel. 25, last sequence update)
D3 16-OCT-2001 (rel. 40, last annotation update)
D4 Unknown protein from 20 page of plasma (Spot 13) (Frappant).
D5 Homo sapiens (Human).
D6 Fokarydai; Metazoa; Chordata; Vertebrata; Eucylostomata;
D7 Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
D8 NCBI_TaxId 9606;
D9 11
D10 SEQUENCE.
D11 TISSUE Plasma;
RX MEDLINE 9409237; PubMed 145097;
R1 Hughes G.L., Frappant S., Papad N., Karpis F., Pasquall C.,
R2 Sanchez J.C., James R., Hsiao J.-D., Hsiao J.-D.,
R3 Hochstetler D.F.;
R4 "Plasma protein map: an update by microsequencing."
R5 Electrophoresis 13:797-714(1992).
R6 1. MISCELLANEOUS: ON THE 20 GEL, THE DELETION OF THIS UNKNOWN
R7 PROTEIN IS: 4.85, 11S MW IS: 40 KDa.
R8 2. MISCELLANEOUS: THIS SPOT IS ON A PAGE 20 THROUGH 10 PAGE THAT ARE
R9 2N ALBUA 2.5VOLUME, BUT IT DOES NOT CORRESPOND TO THAT
R10 PROTEIN.
DR SWISS-PROT: P00911; HUMAN.
FT NON_TER 1
FT VARIANT 9
FT VARIANT 9
FT NON_TER 10
FT SEQUENCE 10 AA: 1109 MW: 64094.732142776 CPG64;

Query Match 21.7% Score 14; DB 1; Length 10;
Best Local Similarity 45.0%; Prot. No. 7e+05;
Matches 2; Conserved 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 KILINR 10
ID 1 1
ID 5 KILINR 10

RESULT 13
CONSEQUENCE
ID CONSEQUENCE STANDARD; PRT; 9 AA.
AC P05486;
D1 01-NOV-1988 (rel. 09, created)

```

```

RP MEDLINE 9209776; PubMed 1726978;
RX Yoshino K, Ito T, Kato T, Shimidzu Y, Suzuki N.
R1 Identification of the amino acid sequence of an intramolecular
R2 disulfide linkage connecting sperm actin and tropomyosin
R3 spectrometry.
R4 FEBS Lett. 294:179-182(1991).
R5 1. FUNCTION: CAUSE INHIBITION OF Sperm PRETREATION AND MOTILITY
R6 THROUGH THE CAUSE OF ALKALINIZING AND CONDENSATION OF
R7 GAMP, FORMING PLASMA MEMBRANE IN SPERM CELLS AND TRANSFER
R8 ACTIVITY AND CONDENSATION TO VACUOLIN AND MEMBRANE FORM
R9 GUANYLATE CYCLASE.
DR PIR: S19329; S19329.
FT DISUFLD 4
SQ SEQUENCE 9 AA: 1010 MW: 64609.087072300 CPG64;

Query Match 21.7% Score 14; DB 1; Length 10;
Best Local Similarity 45.0%; Prot. No. 7e+05;
Matches 2; Conserved 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 KILINR 10
ID 1 1
ID 5 KILINR 10

RESULT 13
CONSEQUENCE
ID CONSEQUENCE STANDARD; PRT; 9 AA.
AC P05486;
D1 01-NOV-1988 (rel. 09, created)

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```

01-NOV-1988 (rel. 09, last sequence update)
01-REV-1994 (rel. 02, last sequence update)
DE LYS-CONOPRESSIN 3.
08 Conus geographus (Geography cone).
06 Eukaryotic Metazoa: Mollusca: Gastropoda: Neritimorpha:
06 Neobornia (Mollusca: Gastropoda: Neritimorpha: Conus).
0X NCBL_Taxid 64933.
0N 111.
0K SEQUENCE.
0X MEDLINE 88078942; PubMed 6600228;
0X Title: De Santos V., Rodriguez C.C., Ramirez C.A., Rodriguez P.L.,
0X Gray W.R., Olivera B.M., Cruz L.J.;
0X "Peptide toxins from venomous Conus snails."
0X Annu. Rev. Biochem. 57:665-700(1988).
02 -1- SIMILARITY: RELIGIONS TO THE VASCOPRESSIN-ANALOG FAMILY.
0X PIR: A28495; A28495.
0X InterPro: IP000081; Neurophysin_hetero.
0X Pfam: PF00220; Hormone4.1.
0X PROSITE: PS00264; NEUROHYPOPHYSIS_HORM; 1.
0X Hormone: Amidation.
0X DISOLEID 1 6 AMINATION.
0X MOD_RES 9 9
0X SEQUENCE 9 AA: 1037 MW: 106276EB154059 C6664.

Query Match 20.0% Score 12; DB 1; Length 9;
Best Local Similarity 66.7% Prod. No. 16-05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

UY 1 CHR 3
1 1
1b 6 CPK 8

RESULT 14
RRPL_PHODV
ID RPLT_PCTV STANDARD PRT 10 AA
AC P35946;
01 01-JUN-1994 (rel. 29, Created)
01 01-JUN-1994 (rel. 29, last sequence update)
01 15-DEC-1998 (rel. 37, last annotation update)
03 RAA Polymers: beta subunit (EC 2.7.7.48) (large structural protein)
0E (1 protein) (Fragment).
0N 1.
0S Phocine distemper virus (PDV).
0S Viruses: ss-RNA: positive strand viruses: %: retroviruses:
0S Paramyxoviridae: Paramyxovirinae: Morbilliviruses.
0X NCBL_Taxid 11248.
0N 111.
0K SEQUENCE FROM N.A.
0X STRAIN-OUTSTR/88.
0X MEDLINE-9226877; PubMed 1588421;
0X Curran M.D., O'Leary D., Kennedy S., Rima B.K.;
0X "Molecular characterization of Phocine distemper virus: gene order
0X RT and sequence of the gene encoding the attachment (H) protein."
0X J. Gen. Virol. 73:1189-1194(1992).
02 -1- FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY
02 FUNCTION IN RNA SYNTHESIS; CAPPING, METHYLATION AND P-GY(A)
02 GENE TRANSCRIPTION, AND PROTEIN KINASE ACTIVITY.
02 -1- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.
02 This SWISS-Prot entry is copyright. It is produced through a collaboration
02 between the Swiss Institute of Bioinformatics and the EMBL institution.
02 The European Bioinformatics Institute. There are no restrictions on its
02 use by non-profit institutions as long as its content is in no way

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02 modified and this statement is not removed. Usage by and for commercial
02 entities requires a license agreement from the EMBL institution.
02 or send an email to license@ebi.ac.uk.
02
02
02
0X MEDLINE 910371; HAN012081;
0X Transcription: RNA-directed RNA polymerase.
0X NCBL 10
0X SEQUENCE 10 AA: 1105 MW: 962876d52f5a2d5 C6664.

Query Match 20.0% Score 12; DB 1; Length 10;
Best Local Similarity 50.0% Prod. No. 1-6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 8 INK 11
1b 6 VNO 9

RESULT 15
RRMK_RANKE
ID RPLT_PCTV STANDARD PRT 10 AA.
AC P56923;
02 16-MAY-2000 (rel. 49, Created)
01 16-OCT-2001 (rel. 49, last sequence update)
01 16-OCT-2001 (rel. 49, last annotation update)
0E Temporalin K.
0S Rana temporaria (European common frog).
0X Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
0X Amphibia: Batrachia: Anura; Neobatrachia: Ranoidae: Rana.
0X NCBL_Taxid-8407;
0N 111.
0K SEQUENCE.
0X STRAIN-OUTSKIN.
0X MEDLINE-9217505; PubMed-9222710;
0X Shimizu M., Mignogna G., Canoteni S., Miele R., Mangoni M.L.,
0X Barra D.;
0X "Temporalin, an antimicrobial peptide from the European red frog Rana
0X temporaria."
0X Eur. J. Biochem. 242:788-792(1996).
02 -1- FUNCTION: HAS ANTI-BACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
02 BACTERIA.
02 -1- SUBCELLULAR LOCATION: Secreted.
02 -1- ACTIVITY: Binds to the cell wall of Gram-positive bacteria.
0X Family.
0X Amphibian skin: Antibiotic: Amidation: Multigene family.
0X MOD_RES 10 10 AMINATION.
0X SEQUENCE 10 AA: 1123 MW: 299549942722452 C6664.

Query Match 20.0% Score 12; DB 1; Length 10;
Best Local Similarity 50.0% Prod. No. 1-6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 5 KIM 8
1b 7 KSL 10

Search completed: July 15, 2002, 14:11:24
Job time: 322 sec

```

1. The first part of the document discusses the importance of maintaining accurate records of all transactions and the role of the accounting system in providing reliable financial information.

2. The second part of the document describes the various methods used to collect and analyze data, including interviews, surveys, and focus groups, and the importance of ensuring the reliability and validity of the data.

3. The third part of the document discusses the results of the study, including the findings of the interviews, surveys, and focus groups, and the implications of these findings for the development of the accounting system.

4. The fourth part of the document discusses the conclusions of the study, including the overall findings and the recommendations for the development of the accounting system, and the importance of ongoing evaluation and improvement.

5. The fifth part of the document discusses the limitations of the study, including the potential biases and limitations of the data collection methods, and the need for further research to address these limitations.

6. The sixth part of the document discusses the future research agenda, including the need for further research to develop and evaluate the accounting system, and the importance of ongoing evaluation and improvement.

7. The seventh part of the document discusses the conclusions of the study, including the overall findings and the recommendations for the development of the accounting system, and the importance of ongoing evaluation and improvement.

8. The eighth part of the document discusses the limitations of the study, including the potential biases and limitations of the data collection methods, and the need for further research to address these limitations.

9. The ninth part of the document discusses the future research agenda, including the need for further research to develop and evaluate the accounting system, and the importance of ongoing evaluation and improvement.

KA MEDLINE 21060601, PubMed 119743119
KA Murphy WJ, Elzirik FK, Johnson W, Ezz Z, Zhao Y, Ali A
of Brunei, Sulu
KA "Molecular Phylogenetics and the Origins of *Flacourtia* in Malaysia"
PL Nature 409:614-616(2001)
PL PMID: 110116257, DOI:10.1038/35011700
PL N. N. 117
PL Sequence: 8 AA: 978 MW: 101003419647224 (2006-1)

Query Match:	45.0%;	Score 27;	108.6;	Length 8;
Best Local Similarity:	80.0%;	Prod. No. 5,60005;		
Matches 4;	conservative 1;	Mismatches 0;	Indels 3;	Gaps 0;

QY	1	CHAK	5
		:	
DB	4	CHKAH	8

[illegible]

Query Match	45.08;	Score 27;	DB 6;	Length 8;
Best Local Similarity	80.08;	Pred. No. 5.6e+05;		
Matches	4;	Conservative	0;	Indels 0;
		Mismatches	0;	Copies 0;

QY	1 CHKAK 5
	11111 ;
100	4 CHKAK: 8

RESID	8	PRELIMINARY:	PRJ:	R AA.
CEBEG				
AD	COBREG			
AN	COBREG			
EL	01 JUN 2001 (TEMPREL: 17, Created)			
EL	01 JUN 2001 (TEMPREL: 17, last sequence update)			
EL	01 JUN 2001 (TEMPREL: 17, last annotation update)			
EL	CAMP RESPONSIVE ELEMENT METHOD (CHAMEN):			
EN	CREM.			
OS	Myxococcal flagella (glut autoant)			
OS	Electrostatic Motility of Chemotaxis (Glutamate) With Glutamate			
OS	Myxococcal flagella: Glutamate (Glutamate) With Glutamate			
OX	NBI_TaxID:71006;			
RI	11			
RP	SEQUENCE FROM N.A.			
EX	MEDLINE 21922082; PubMed 12111119;			
KA	Murphy W.L., Electric E., Schmitt W.L., Chan Y.F., Byrd J.A.,			
KA	W. Chan S.J.;			
RI	"Molecular phylogenetics and the origins of placental mammals."			
RI	Nature 409:614-618(2001).			

EN 1982, AYO1927, AAO37542.1) -
ET NUMBER 1
SU SPONSOR: HAO, 978 RW, 4F110331EHA05720 CR064

Query Match:	45.08;	Score 27;	DB 6;	Length 8;
Best Local Similarity	80.08;	Pred. No. 5;	Occ ² 5;	
Matches	4;	Conservative	1;	Mismatches 0;
				Indels 0;
				Gaps 57;

QY	1 CHKAK :
Db	1111 :
	4 CHKAF :

Q9RFB5	9	PRELIMINARY;	PRT:	8 AA.
1D	Q9RFB5			
AC	Q9RFB5			
Q9RFB5				
01 JUN 2001	(11EMBL01_17, created)			
01 JUN 2001	(11EMBL01_17, last sequence update)			
01 JUN 2001	(11EMBL01_17, last annotation update)			
2AB	SLC1A5 (SLC1A5) (HUMAN)			
GN	SLC1A5			
OS	Homo sapiens (Homo sapiens)			
OR	Brain			
OX	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
ON	Mammalia; Eulipotyria; Insectivora; Eulipotyria; Eulipotyria;			
NC	Protein; Amino acid; 447; 447;			
KN	111			
RP	SH000007 (From N.A.)			
KX	SH000007 (From N.A.)			
FA	SH000007 (From N.A.)			
KA	SH000007 (From N.A.)			
RL	SH000007 (From N.A.)			
RE	SH000007 (From N.A.)			
TE	SH000007 (From N.A.)			
SD	SH000007 (From N.A.)			

Query Match	45.0%	Score 27	DB 6	Length 8
Best Local Similarity	80.0%	Prod. No.	5	Go:05
Matches	1	Conservative	1	Mismatches 0
				Gaps 0

QY	1 CHAK
DB	4 CHAK: 8

RESULT	10	
C9B9F4		
10	C9B9F4	PRELIMINARY: PRT: 8 AA.
AC	C9B9F4:	
D7	01-JUN-2001 (TEEMEROL_17, Created)	
D9	01-JUN-2001 (TEEMEROL_17, Last sequence update)	
D1	01-JUN-2001 (TEEMEROL_17, Last annotation update)	
D4	C9B9: REGENERATIVE ELEMENT REGENERATOR (PRA:BMN1).	
D6	C9B9:	
D8	Laipa alitica (Silurian mole).	
06	Eukaryota: Metazoa: Chordata: Gracilaria: Vertebrata: Euteleostomi:	
0C	Mammalia: Eutheria: Insectivora: Talpidae: Talpa.	
0X	PRT: L04D 114409:	
0X	[1]	
KN	SEQUENCE FROM N.A.	
RP	MM110H 21082662: PubMed 1121419:	
FX	Murphy, W.J., Elstrik E., Johnson W.E., Zhang Y.P., Ryder O.A.,	
FA	et al. 2001.	
EA	Journal Sci.	
RT	"Molecular phylogenetics and the origins of placental mammals."	
RL	Nature 409:614-618(2001).	
ISB	EMBL: AY014529; Acc:375544.1.	
LT	NCBI: 1	
SD	SEQUENCE: 8 AA: 978 MW: DF110341EAF572A 16064:	

Query Match	45.08%	Score 27	DB 6	Length 8
Best Local Similarity	80.00%	Prod. No. 5.6005		
Matches	4	Conservative	0	Indels
		Mismatches	0	Gaps

BY	1	11KAK	4
		111	
BY	4	11KAK	8

Seq	Accession	Gene	Species	Ref.	AA
1	U00096.1	REP1	<i>Escherichia coli</i>	11	
2	U00096.1	REP1	<i>Escherichia coli</i>	11	
3	U00096.1	REP1	<i>Escherichia coli</i>	11	
4	U00096.1	REP1	<i>Escherichia coli</i>	11	
5	U00096.1	REP1	<i>Escherichia coli</i>	11	
6	U00096.1	REP1	<i>Escherichia coli</i>	11	
7	U00096.1	REP1	<i>Escherichia coli</i>	11	
8	U00096.1	REP1	<i>Escherichia coli</i>	11	
9	U00096.1	REP1	<i>Escherichia coli</i>	11	
10	U00096.1	REP1	<i>Escherichia coli</i>	11	
11	U00096.1	REP1	<i>Escherichia coli</i>	11	
12	U00096.1	REP1	<i>Escherichia coli</i>	11	
13	U00096.1	REP1	<i>Escherichia coli</i>	11	
14	U00096.1	REP1	<i>Escherichia coli</i>	11	
15	U00096.1	REP1	<i>Escherichia coli</i>	11	
16	U00096.1	REP1	<i>Escherichia coli</i>	11	
17	U00096.1	REP1	<i>Escherichia coli</i>	11	
18	U00096.1	REP1	<i>Escherichia coli</i>	11	
19	U00096.1	REP1	<i>Escherichia coli</i>	11	
20	U00096.1	REP1	<i>Escherichia coli</i>	11	
21	U00096.1	REP1	<i>Escherichia coli</i>	11	
22	U00096.1	REP1	<i>Escherichia coli</i>	11	
23	U00096.1	REP1	<i>Escherichia coli</i>	11	
24	U00096.1	REP1	<i>Escherichia coli</i>	11	
25	U00096.1	REP1	<i>Escherichia coli</i>	11	
26	U00096.1	REP1	<i>Escherichia coli</i>	11	
27	U00096.1	REP1	<i>Escherichia coli</i>	11	
28	U00096.1	REP1	<i>Escherichia coli</i>	11	
29	U00096.1	REP1	<i>Escherichia coli</i>	11	
30	U00096.1	REP1	<i>Escherichia coli</i>	11	
31	U00096.1	REP1	<i>Escherichia coli</i>	11	
32	U00096.1	REP1	<i>Escherichia coli</i>	11	
33	U00096.1	REP1	<i>Escherichia coli</i>	11	
34	U00096.1	REP1	<i>Escherichia coli</i>	11	
35	U00096.1	REP1	<i>Escherichia coli</i>	11	
36	U00096.1	REP1	<i>Escherichia coli</i>	11	
37	U00096.1	REP1	<i>Escherichia coli</i>	11	
38	U00096.1	REP1	<i>Escherichia coli</i>	11	
39	U00096.1	REP1	<i>Escherichia coli</i>	11	
40	U00096.1	REP1	<i>Escherichia coli</i>	11	
41	U00096.1	REP1	<i>Escherichia coli</i>	11	
42	U00096.1	REP1	<i>Escherichia coli</i>	11	
43	U00096.1	REP1	<i>Escherichia coli</i>	11	
44	U00096.1	REP1	<i>Escherichia coli</i>	11	
45	U00096.1	REP1	<i>Escherichia coli</i>	11	
46	U00096.1	REP1	<i>Escherichia coli</i>	11	
47	U00096.1	REP1	<i>Escherichia coli</i>	11	
48	U00096.1	REP1	<i>Escherichia coli</i>	11	
49	U00096.1	REP1	<i>Escherichia coli</i>	11	
50	U00096.1	REP1	<i>Escherichia coli</i>	11	

Query Match:	45.08	Score 27	DB 6	Length 87
Best Local Similarity:	60.08	Pred. No.	5.6e-05	
Matches	4	Conservative	1	Mismatches
			0	Indels
			0	Gaps

1	CHKAK	1	CHKAK
2	CHKAK	2	CHKAK
3	CHKAK	3	CHKAK
4	CHKAK	4	CHKAK
5	CHKAK	5	CHKAK
6	CHKAK	6	CHKAK
7	CHKAK	7	CHKAK
8	CHKAK	8	CHKAK
9	CHKAK	9	CHKAK
10	CHKAK	10	CHKAK
11	CHKAK	11	CHKAK
12	CHKAK	12	CHKAK
13	CHKAK	13	CHKAK
14	CHKAK	14	CHKAK
15	CHKAK	15	CHKAK
16	CHKAK	16	CHKAK
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18	CHKAK	18	CHKAK
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21	CHKAK	21	CHKAK
22	CHKAK	22	CHKAK
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25	CHKAK	25	CHKAK
26	CHKAK	26	CHKAK
27	CHKAK	27	CHKAK
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29	CHKAK	29	CHKAK
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31	CHKAK	31	CHKAK
32	CHKAK	32	CHKAK
33	CHKAK	33	CHKAK
34	CHKAK	34	CHKAK
35	CHKAK	35	CHKAK
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96	CHKAK	96	CHKAK
97	CHKAK	97	CHKAK
98	CHKAK	98	CHKAK
99	CHKAK	99	CHKAK
100	CHKAK	100	CHKAK

	RESULT	1.2	CORRECT	PRELIMINARY:	PREP.	R.AA.
D0	OTHERC:					
A*	OTHERC:					
D1	01 JUN 2001 (ITERMID-17, created)					
E*	01 JUN 2001 (ITERMID-17, last sequence update)					
F*	01 JUN 2001 (ITERMID-17, last annotation update)					
DE	CAMP RESPONSIVE ELEMENT MECHANISM (CREM).					
EN	CREM.					
ES	FOURCAT atonous (fourAsian common shrew) (European shrew);					
ET	Slovakia; Molodtsov; Obukhov; Orlovskaya; Vokoschinskii;					
EX	Mammalia; Eutheria; Insectivora, Soricidae, Sorex.					
CO	NBRL TAXID 42254;					
CP	ILIT					
KP	SEQUENCE FROM R.A.					
BX	MEHLINIE_21082002; pubmed 11214319;					
BA	Murphy W.F., Fitzpatrick E., Johnson W.P., Zhang Y.L., Kyte J., Auer					
KA	Johnson S.D.;					
RI	"Molecular phylogenies and the origins of placental mammals";					
EL	Nature 406:614-618(2001).					
EMH:	AY011641; AAC01944.1 - -					
LK	NON_LTR					
FI	1					
SD	STUDENTS: R.AA: 978 BM: 1010031LEAF572A ORV4:					

query Match	45.0%	Score 27	106.61	Length 92
Post local Similarity	50.0%	Prod. No.	5.6e+05	
Matches	47	Conserved	17	Mismatches
			02	Gaps
			02	

1000

PH 4 71KAE 8

[illegible]

Query Match	45.08	Score 27	136	Length 8					
Best Local Similarity	80.06	Pred. No.	5,560	95					
Matches	4	Conservative	1	Mismatches	0	Indels	0	Gaps	0

4. **TRKAF: H**

[illegible]

Query Match	45.00%	Score 27	144	Length 81
Post Local Similarity	80.00%	Prod. No.	5,000,000	
Matches	4	Conservative	1	Mismatches
			0	Indels
			0	Upd

Учредитель: И. И. И. И. И.

RESULTS

RESULTS

Q9BFA9
 ID Q9BFA9 PRELIMINARY PKT: 8 AA.
 AC Q9BFA9
 DI 01-JUN-2001 (TEMBREL: 17, Created)
 DI 01-JUN-2001 (TEMBREL: 17, Last sequence update)
 DI 01-JUN-2001 (TEMBREL: 17, Last annotation update)
 DE CAMP RESPONSIVE ELEMENT MODERATOR (FRAGMENT).
 GN CREM.
 OS *Procapra capensis* (Gape Hyrax) (Pock dassie).
 OC Euparotia: Molozoa: Chordata: Crataei: Vertebrata: Euteleostomi:
 OC Mammalia: Proboscidea: Afrotheria: Proboscidea: Elephantia.
 OX NCBI_TaxID 9813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 21082922, PubMed 11214319,
 RA Murphy W.T., Flicsik E., Johnson W.E., Chang Y.F., Egdé, A.,
 RA O'Brien S.J.;
 RT "Molecular phylogenetics and the origins of placental mammals."
 RL Nature 409:614-616(2001).
 DR EMBL: AY011634; AAC47549.1; -;
 FI NNN_NNN 1
 FI NNN_NNN 1
 SQ SEQUENCE 8 AA: 978 MW: 10100321EFA8572A CR064;

Query Match 45.08; Score 27; 18 6; Length 8;
 Best Local Similarity 80.08; Pred. No. 5.6e-05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHKA 5
 Db 4 CHKA 8

Search completed: July 15, 2002, 14:11:04
 Job time: 357 sec

1

CC Preventing other growth of cardiac and vascular tissue.
 XX
 S2 Sequence 9 AA;

Query Match 43.48% Score 26; DB 21; Length 9;
 Best Local Similarity 55.58% Pred. No. 6,4e+05;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CHKAKIMLN 9
 I I I I I
 DB 1 CHKAKIMLN 9

RESULT 6
 AAB66508
 ID AAB66508 standard; Peptide: 9 AA.
 XX
 AC AAB66508;

DE 10 APR-2001 (first entry)
 XX
 DE Human NF-ATc1 putative NLS #1.

XX
 KM Human nuclear factor of activated T lymphocytes, NF-ATc1,
 NF-ATc1 cytoplasmic component, NP-ATc1, NF-ATc1 transactivator
 XX nuclear localization sequence; NLS; SRK.

OS Homo sapiens.

PN OS6171701.1.

PD 09 JAN 2001.

PT 27 MAR 1998; 980S-0340691.

PR 28 SEP 1999; 980S-0124981.

PR 18 JUN 1994; 980S-0260174.

PR (SIRK) UNIV LUTLAND, STAMP-60; UNK 98.

PI Cloning 38; Northern 37; Bio. Sci.

DE WPI: 2001.122428/13.

XX
 PI Screening assay for identifying modulators of translocation of nuclear
 PI factor of activated T lymphocytes across nuclear membrane of cell, by
 PI fraction with nuclear factor of activated T lymphocyte polypeptide

XX
 PI Claim 1; Fig 1A; 99pp; English.

XX
 CC The present sequence is given in a specification related to a method for
 CC identifying a compound which modulates translocation of a nuclear factor
 CC of activated T lymphocytes (NF-AT) polypeptide across the nuclear
 CC membrane of a cell. The method involves binding the compound to the
 CC NF-AT polypeptide. The method is useful for identifying compounds which
 CC modulate nuclear translocation of NF-AT present in the cytoplasm and/or
 CC in the nucleus of the cell, and for identifying agents that modulate
 CC phosphorylation/dephosphorylation of NF-AT.

XX
 S2 Sequence 9 AA;

Query Match 43.48% Score 26; DB 22; Length 9;
 Best Local Similarity 55.58% Pred. No. 6,4e+05;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CHKAKIMLN 9
 I I I I I
 DB 1 CHKAKIMLN 9

RESULT 7

AAB31772
 ID AAB31772 standard; peptide: 10 AA.
 XX
 AC AAB31772;

DE 30-APR-2001 (first entry)

XX
 DE Amino acid sequence of a cross linking peptide.

XX
 KM Nucleic acid condensate; cationic linker; gene therapy.

XX
 OS Synthetic.

PN WC200104135-A2.

PD 18-JAN-2001.

PR 13-JUL-2000; 2000WO 0819164.

PR 13-JUL-1999; 990S-014600.

PR 05-OCT-1999; 990S-0157761.

PA (UNMI) UNIV MICHIGAN.

XX
 PI Rice KS, Adams RJ, Mendez LL, Colvard WJ, Swick KL, Park YJ
 PI Yang Y;

DE WPI: 2001-168410/17.

XX
 PI Compositions comprising nucleic acid condensates having a nucleic acid
 PI bound to two low molecular weight cationic linkers, used in human gene
 PI therapy, and diagnostics

XX
 PI Claim 1; Page 152; 204pp; English.

XX
 CC The specification describes a composition comprising a nucleic acid
 CC condensate. This condensate comprises a nucleic acid bound to two low
 CC molecular weight cationic linkers. The linkers are crosslinked to each
 CC other by reaction with a low molecular weight dialdehyde. Alternatively,
 CC the linkers each contain at least two thiol groups and are crosslinked
 CC by reaction of the thiol groups. The low molecular weight carriers are
 CC minimal in size, reduce toxicity, condense DNA into small particles,
 CC have increased stability, and mediate effective gene expression in a
 CC target tissue. The nucleic acid condensate is used for gene therapy,
 CC particularly human gene therapy, and diagnostics. It is also used for
 CC expressing nucleic acids in cells and providing a nucleic acid to an
 CC animal. The present sequence represents a cross-linking peptide, which
 CC is used as a linker in the composition of the invention. The peptide
 CC condenses DNA.

XX
 S2 Sequence 10 AA;

Query Match 43.48% Score 26; DB 22; Length 10;
 Best Local Similarity 80.00% Pred. No. 1,9e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CHKAK 5
 I I I I
 DB 1 CHKAK 5

RESULT 8

AAB31773
 ID AAB31773 standard; peptide: 10 AA.

XX
 AC AAB31773;

DE 30-APR-2001 (first entry)

XX
 DE Amino acid sequence of a cross-linking peptide.

XX
 KM Nucleic acid condensate; cationic linker; gene therapy.

Query Match 40.0%; Score 24; DB 20; Length 92
 Best Local Similarity 57.1%; Pred. No. 6.4e+05;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 5 KTMUNRI 11
 1 1111
 Db 3 Kdlunv 9

RESULT 13
 AAY84122
 ID AAY84122 standard; Peptide: 10 AA.
 XX
 AC AAY84122;
 XX
 DE 04-JUN-2000 (first entry)
 DE Peptide used to derive a PCR primer for cloning human hsp5.
 XX
 KW Human; hsp5; DNA; DNA related protein; gene therapy;
 KW differential screening selected gene; Abbreviation: In Neuroblastoma;
 KW bone morphogenetic protein; BMP-binding protein; cartilage growth;
 KW bone growth.
 XX
 OS Homo sapiens.
 XX
 FN W020001153-A1.
 XX
 PD 02-MAR-2000.
 XX
 PE 12-APR-1999; 9900-0517979.
 XX
 PR 20-AUG-1998; 9808-0097296.
 XX
 PA (REGG-) REGENERON PHARM INC.
 XX
 PT Reonomides AN, Stahl N;
 XX
 DB WP1: 2300-224698/19.
 XX
 DB N-PSDB: AAZ952641.
 XX
 P1 Isolated nucleic acids encoding human DCR5, useful for production
 P1 cartilage and bone growth by administering bone growth factor proteins -
 XX
 PS Example 1; Page 16; 34pp; English.
 XX
 DE Peptides AAY84122 were used to derive PCR primers AAY84122-65, which
 DE were used to amplify cDNA encoding human hsp5, which was then related
 DE to DAN (differential screening selected gene; Abbreviation: In
 DE Neuroblastoma), and is a bone morphogenetic protein (BMP) binding
 DE protein. The DCR5 protein antagonizes bone morphogenetic protein. The
 DE hsp5 nucleic acids may be used for the recombinant production of human
 DE hsp5 either in vitro (as a fermentation culture) or in vivo as part of a
 DE gene therapy protocol. The protein may be used to either supplement a
 DE patient's own production of DCR5 or rectify mutations that lead to the
 DE expression of an inactive peptide. The proteins may also be used as
 DE antigens for the production of antibodies specific for hsp5. The
 DE antibodies may be used to down regulate hsp5 activity or as diagnostic
 DE reagents for detecting and quantifying hsp5 proteins in samples according
 DE to standard recombinant DNA methodologies. The proteins and antibodies
 DE may be used to regulate cartilage and bone growth.
 XX
 SO Sequence 10 AA;

Query Match 40.0%; Score 24; DB 21; Length 100
 Best Local Similarity 57.1%; Pred. No. 1.6e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 4 AKTMNR 10
 1 11111
 Db 1 stllnr 7

RESULT 14
 AAG85901
 ID AAG85901 standard; Peptide: 10 AA.
 XX
 AC AAG85901;
 XX
 DE 11-SEP-2001 (first entry)
 DE Saccharomyces cerevisiae peptide; SEQ ID NO: 850.
 XX
 KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
 KW drug discovery; drug design.
 XX
 OS Saccharomyces cerevisiae.
 XX
 FN W020014276-A1.
 XX
 PD 14-JUN-2001.
 XX
 PE 14-DEC-2000; 2000W0-GB04773.
 XX
 PR 13-DEC-1999; 99CB-0029471.
 XX
 PA (PROT-) PROTEOM LTD.
 XX
 PT Roberts GW, Hoal JR;
 XX
 DB WP1: 2301-96796/338.
 XX
 P1 Identifying complementary peptides by analysis of protein and
 P1 nucleotide sequence databases, useful in drug design -
 XX
 PS Example 3; Page 147; 488pp; English.
 XX
 DE The invention relates to the identification of complementary peptides
 DE by analysis of protein and nucleotide sequence databases from higher
 DE eukaryotic genomes, excluding human and plants. The specific
 DE complementary peptides interact with their relevant target proteins
 DE encoded in the eukaryotic genome. The peptides may be used as reagents
 DE and drugs for drug discovery and as food ligands for drug design and
 DE development. The present sequence is a complementary peptide from
 DE Saccharomyces cerevisiae.
 XX
 SO Sequence 10 AA;

Query Match 40.0%; Score 21; DB 23; Length 100
 Best Local Similarity 44.4%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CHAKTMNR 9
 1 1 1 1
 Db 2 ckrctmnr 10

RESULT 15
 AAG85903
 ID AAG85903 standard; Peptide: 10 AA.
 XX
 AC AAG85903;
 XX
 DE 11-SEP-2001 (first entry)
 DE Saccharomyces cerevisiae peptide; SEQ ID NO: 852.
 XX
 KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
 KW drug discovery; drug design.
 XX
 OS Saccharomyces cerevisiae.
 XX
 FN W020014276-A1.

```

XX      14 JUN-2001.
XX      15 DEB-2000: 2000W-00004774.
XX      15 DEB-1999: 990B-0020171.
XX      (Prot.) PROTEOM LTD.
XX      Roberts CW, Heal JK:
XX      WPI: 2001-367863/38.
XX      Identifying complementary peptides by analysis of protein and
XX      nucleotide sequence databases, useful in drug design -
XX      Example 4: page 147; 488pp; English.
XX
XX      The invention relates to the identification of complementary peptides
XX      by analysis of protein and nucleotide sequence databases from higher
XX      eukaryotic genomes, excluding human and plants. The specific
XX      complementary peptides interact with their relevant target proteins
XX      encoded in the eukaryotic genome. The peptides may be used as reagents
XX      and drugs for drug discovery and as lead ligands for drug design and
XX      development. The present sequence is a complementary peptide from
XX      Saccharomyces cerevisiae.
XX      Sequence: 10 AA:
XX
XX      Query Match: 40 0%; Score 24; DH 22; Length 10
XX      Post Local Similarity: 44 1%; Pred. No. 4,600,027
XX      Matches: 4; Conservative: 0; Mismatches: 6; Indels: 0; Gaps: 0
XX
XX      QY      1 CHKAKIMLN 9
XX              1 1 1 1
XX      DB      2 cckvstgqn 10

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Search completed: July 15, 2002, 14:06:00
 Job time: 188 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Computer Corp.

OM protein - protein search, using sw model

Run on: July 15, 2002, 14:06:26 ; Search time 20.17 seconds
(without alignment)

13.126 Million cell updates/sec

Title: US-09-719-053A-5

Perfect score: 60

Sequence: 1 CHXATM NP1 11

Scoring table: BLISSUM62

Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 76579

Minimum DB seq length: 0

Maximum DB seq length: 11

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents, AA:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	48.1	10	US-08-454-207A-3	Sequence 3, Appl
2	29	48.1	10	US-08-454-207A-6	Sequence 6, Appl
3	26	43.1	9	US-08-049-691-53	Sequence 53, Appl
4	23	38.1	9	US-08-049-691-16	Sequence 16, Appl
5	22	36.1	6	US-09-235-246-6	Sequence 6, Appl
6	22	36.1	8	US-08-482-228-46	Sequence 46, Appl
7	22	36.1	8	US-08-482-228-46	Sequence 46, Appl
8	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
9	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
10	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
11	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
12	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
13	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
14	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
15	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
16	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
17	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
18	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
19	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
20	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
21	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
22	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
23	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
24	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
25	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
26	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
27	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
28	22	36.1	9	US-08-482-228-46	Sequence 46, Appl
29	22	36.1	9	US-08-482-228-46	Sequence 46, Appl

28	21	35.0	11	5	PCT-US95-11445-20	Sequence 20, Appl
29	20	32.3	5	2	US-09-244-496-36	Sequence 36, Appl
30	20	33.3	5	2	US-07-616-910-2	Sequence 2, Appl
31	20	33.3	6	5	PCT-US91-08497-2	Sequence 2, Appl
32	19	31.7	4	2	US-08-350-260A-400	Sequence 400, App
33	19	31.7	5	4	US-08-392-512-21	Sequence 21, Appl
34	19	31.7	5	4	US-08-894-227-21	Sequence 21, Appl
35	19	31.7	6	4	US-09-128-572-39	Sequence 39, Appl
36	19	31.7	6	4	US-09-426-568A-8	Sequence 8, Appl
37	13	31.7	7	1	US-08-160-343-15	Sequence 15, Appl
38	19	31.7	7	1	US-08-328-256-4	Sequence 4, Appl
39	19	31.7	7	2	US-08-727-045A-15	Sequence 15, Appl
40	19	31.7	7	4	US-09-128-572-32	Sequence 32, Appl
41	19	31.7	7	4	US-09-128-572-39	Sequence 39, Appl
42	19	31.7	7	4	US-09-128-572-45	Sequence 45, Appl
43	19	31.7	7	5	PCT-US94-01234-41	Sequence 41, Appl
44	19	31.7	7	6	US-09-128-572-25	Sequence 25, Appl
45	19	31.7	8	4	US-09-128-572-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-08-454-207A-3
Sequence 3, Appl
Patent No. 5710123
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
INVENTOR: Kruszynski, Marian
ATTORNEY: W. J. Kruszynski, 70
ADDRESS: 10000 W. 10th Ave., Suite 100, Denver, CO 80202
STATE: CO
COUNTRY: U.S.A.
ZIP: 80202
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08-454-207A
FILING DATE: 09 JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-08-454-207A
FILING DATE: 13 DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/997,771
FILING DATE: 16 DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/OTHER NUMBER: 0208-0183
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-454-207A-3

Query Match: 48.38, Score 29, DB 1, Length 10;
Best Local Similarity: 62.58, Pred. No. 17;
Matches: 9, Conserved: 6, Missed: 0, Gaps: 0;

QY 1 CIRKATML 8
DB 1 CIRKATML 8

RESULT 2
US-08-454-207A-6
Sequence 6, Application US/08454207A
Patent No. 5710123
GENERAL INFORMATION:
APPLICANT: HOVART, George A.
APPLICANT: KRZYWINSKI, Marian
TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSER: Westock Warehouse, Route 200, 07102-2010, NJ
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER REAMABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09-454-207A
FILING DATE: 09-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12113
FILING DATE: 13-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/997,771
FILING DATE: 18-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/AGENT INFORMATION:
TELEPHONE: 215-568 4400
TELEFAX: 215-568 4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
POLARITY: circular
US-08-454-207A-6

Query Match 48.3%; Score 29; DB 1; Length 10;
Best local similarity 62.5%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CIRKATML 8
DB 1 CIRKATML 8

RESULT 3
US-09-049-691-53
Sequence 53, Application US/09049691
Patent No. 6171781
GENERAL INFORMATION:
APPLICANT: Crabbtree, Gerald R.
APPLICANT: Ho, Stephen M.
TITLE OF INVENTION: NP AT POLYPEPTIDES AND POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: PULLEY, 4000 N. 40th St, 48106
CITY: Detroit, MI 48206
STATE: MI
COUNTRY: U.S.A.
ZIP: 48206
COMPUTER REAMABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09-049-691-53
FILING DATE: 09-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12113
FILING DATE: 13-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/997,771
FILING DATE: 18-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/AGENT INFORMATION:
TELEPHONE: 215-568 4400
TELEFAX: 215-568 4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
POLARITY: circular
US-08-454-207A-6

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER REAMABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patcud Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09-049-691
FILING DATE: 27-MAR-1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,174
FILING DATE: 13-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,981
FILING DATE: 20-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 46,709
REFERENCE/AGENT INFORMATION:
TELEPHONE: 617-832-7000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLARITY: linear
MOLECULE TYPE: peptide
US-09-049-691-53

Query Match 43.3%; Score 26; DB 4; Length 9;
Best local similarity 55.6%; Pred. No. 17; Indels 9; Gaps 0;
Matches 5; Conservative 1; Mismatches 3; Indels 9; Gaps 0;

QY 1 CIRKATML 9
DB 1 CIRKATML 9

RESULT 4
US-08-435-925C-16
Sequence 16, Application US/08435925C
Patent No. 5646025
GENERAL INFORMATION:
APPLICANT: Moyer, Donna
TITLE OF INVENTION: SCYLLADIN CATALASE GENE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSER: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER REAMABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patcud Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-435-925C
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 41,728
REFERENCE/AGENT INFORMATION:
TELEPHONE: 4129,000-05

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-862-0123
TELEFAX: 212-878-9655
INFORMATION FOR C/D: 15, 16.
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STEREODNESS: single
TOPOLOGY: linear
US-09-425-9253-16

Query Match 38.38% Score 23; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 17e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 TMNRI 11
11111
DB 4 TOLNRY 9

RESULT 5
US-09-235-246-6
Sequence 5, Application US/09235246A
Patent No. 6048719
GENERAL INFORMATION:
APPLICANT: Kong, Hui-min
APPLICANT: Hsiao, Joun-S
APPLICANT: Dalton, Michael A.
TITLE OF INVENTION: Method For Cloning And Producing The Dna11 Protein
FILE REFERENCE: DRA11
CURRENT APPLICATION NUMBER: US/09/235-246A
CURRENT FILING DATE: 1999-01-22
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patent In Ver 2.0
SEQ ID NO: 6
LENGTH: 6
TYPE: PRT
ORGANISM: Deinococcus radiophilus
US-09-235-246-6

Query Match 36.7% Score 22; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 17e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHR 3
111
DB 4 CHR 6

RESULT 6
US-08-482-228-49
Sequence 19, Application US/0848228
Patent No. 5968753
GENERAL INFORMATION:
APPLICANT: Tseng, Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Holgerson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND NEGATIVE/NEGATIVE CELL
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210

COMPUTER READABLE FORM:
MEDIA TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482-228
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-08-482-228-49

Query Match 36.7% Score 22; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 17e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHR 3
111
DB 5 CHR 7

RESULT 7
US-08-482-528-49
Sequence 49, Application US/08482528
Patent No. 6017719
GENERAL INFORMATION:
APPLICANT: Tseng, Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Holgerson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND NEGATIVE/NEGATIVE CELL
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
MEDIA TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482-528
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:

1 LENGTH: 8 amino acids
2 TYPE: amino acid
3 TOPOLOGY: linear
4 MOLECULE TYPE: peptide
5 US-08-482-651-19

Query Match 46.7% Score 22, DB 3, Length 9
Best Local Similarity 10.0% Prod. No. 176-05
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CHK 3
DB 5 CHK 7

RESULT 8

US-08-482-651-19
Sequence 19, Application US/08482651

Patent No. 5874409

GENERAL INFORMATION:

APPLICANT: Victor I., Edward J.

APPLICANT: Marquis, David M.

TITLE OF INVENTION: AN IMMUNO-REACTIVE PEPTIDES, COMPOUNDS

TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDES, COMPOUNDS

TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDES, COMPOUNDS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: MERRILL & PIERCE

STREET: 765 FINE HILL ROAD

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

ZIP: 94004-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482-651

FILING DATE: 07 JUN 1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Park, Fredrick K.

REGISTRATION NUMBER: 49,496

REFERENCE: 1722-2799, 2723-2799, 2799-1,000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 943-5600

TELEFAX: (415) 943-0792

TELEX: 706111

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: xyz (details pt. 16)

CLONE: 488

US-08-482-651-19

Query Match 46.7% Score 22, DB 4, Length 9
Best Local Similarity 10.0% Prod. No. 176-05
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CHK 3
DB 1 CHK 3

RESULT 9

US-08-986-234-45
Sequence 45, Application US/08986234

Patent No. 5981706

GENERAL INFORMATION:

APPLICANT: Wallen, et al.

TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Compounds

FILE REFERENCE: UNRE-0008-1

CURRENT APPLICATION NUMBER: 08/086,234

CURRENT FILING DATE: 1997-12-05

NUMBER OF SEQ ID NOS: 114

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 45

LENGTH: 9

TYPE: PR

ORGANISM: Human Immunodeficiency Virus

US-08-986-234-45

Query Match 36.7% Score 22, DB 2, Length 9
Best Local Similarity 66.7% Prod. No. 176-05
Matches 4: Conservative 1: Mismatches 1: Indels 0: Gaps 0:

QY 6 MINUT 11
DB 4 MINUT 9

RESULT 10

US-08-159-199A-567

Sequence 567, Application US/08159199A

Patent No. 6037135

GENERAL INFORMATION:

APPLICANT: Kubo, Ralph L.

APPLICANT: Gray, Edward M.

APPLICANT: Setto, Alessandro

APPLICANT: Gellis, Estaban

TITLE OF INVENTION: HIV Binding peptides and their

TITLE OF INVENTION: HIV Binding peptides and their

NUMBER OF SEQUENCES: 1254

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crow LLP

STREET: Two Embarcadero Center, Eleventh Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-4834

COMPUTER READABLE FORM:

MEDIUM TYPE: diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 08/086,234

FILING DATE: 29-Nov-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

FILING DATE: 07-06-1992

APPLICATION NUMBER: US 08/027,746

FILING DATE: 05-MAR-1993

APPLICATION NUMBER: US 08/103,396

FILING DATE: 06-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lawlor

REGISTRATION NUMBER: 42,762

TELEPHONE: (415) 776-0000

TELEFAX: (415) 576-0000

TELEX: (415) 576-0000

INFORMATION FOR SEQ ID NO: 567:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-359A-667

Query Match 35.7% Score 22 DB 4 Length 9
Host Local Similarity 100.0% Pred. No. 1.7e+05
Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

RESULT 11
US-08-660-092-22
Sequence 22, Application US/08660092
Patent No. 6207160
GENERAL INFORMATION:
APPLICANT: Victoria, Edward J.
APPLICANT: Margolis, David M.
APPLICANT: Jones, David S.
APPLICANT: Y. 16
TITLE OF INVENTION: gtl. IMMUNOREACTIVE PEPTIDES & ANALOGS
TITLE OF INVENTION: THERE-OF ARE METHODS OF TREATMENT FOR gtl. ANTIBODY MEDIATED
TITLE OF INVENTION: PATHOLOGIES
NUMBER OF SEQUENCES: 216
CORRESPONDENCE ADDRESS:
ADDRESS: Morrison & Prosser
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: us-08-660-092
FILING DATE: 06-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Park, Freddie K.
REGISTRATION NUMBER: 35,636
REFERENCE/CHECK NUMBER: 25231-20061.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE
LIBRARY: xyz (details pg. 16)
CLONE: 4F8
IS-08-660-092-22

Query Match 36.7% Score 22 DB 4 Length 9
Host Local Similarity 100.0% Pred. No. 1.7e+05
Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

Y 1 CRK 3
111
DB 1 CRK 3

RESULT 12
US-08-444-818-470

Sequence 6, Application US/08366591
Patent No. 5602021
GENERAL INFORMATION:
APPLICANT: Davis, G. Claude
APPLICANT: Garry, Gordon G.
TITLE OF INVENTION: Method for generating proteolytic
TITLE OF INVENTION: Enzymes Specific Against a Selected Peptide Sequence
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: us-08-444-818-470
FILING DATE: 29-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shultz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/CHECK NUMBER: 2292-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 424-0880
TELEFAX: (415) 424-0960
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-444-818-470

Query Match 36.7% Score 22 DB 1 Length 10
Host Local Similarity 50.0% Pred. No. 3.3e+02
Matches 4 Conservative 2 Mismatches 2 Indels 0 Gaps 0

Y 2 HRAKMLN 9
111111
DB 1 HSAETLID 8

RESULT 13
US-08-444-818-470
Sequence 470, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rottier, William J.
TITLE OF INVENTION: NARROW Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESS: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: 05-200-2408-560
3 FILING DATE: 14 MAR 1995
4 CLASSIFICATION: 424
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 05-200-2408-560
7 FILING DATE: 14 MAR 1995
8 ATTORNEY/AGENT INFORMATION:
9 NAME: BARBIO, A USA A
10 REGISTRATION NUMBER: 44,895
11 REFERENCE: 211,002
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: (508) 359 3876
14 TELEFAX: (508) 359 3885
15 INFORMATION FOR SEQ ID NO: 470:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 8 amino acids
18 TYPE: amino acid
19 STRANDEDNESS: single
20 ORIENTATION: forward
21 MOLECULE TYPE: peptide
22 DS: 04 444 B18 470

```

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Query Match 35.0% Score 21: DB 4: Length 8:
Host Local Similarity 62.5%: Prod. No. 1.7e+05:
Matches 5: Conservative 0: Mismatches 4: Indels 0: Gaps 0:
UY 4 AKIMNRI 11
DB 1 AKIMNRI 8

```

```

RESULT 14
US-09-128-572-27
1 Sequence 27, Application US/09128572
2 Patent No. 6,251,866
3 GENERAL INFORMATION:
4 APPLICANT: FRUKASH, Karest K.
5 TITLE OF INVENTION: (2) mutations targeted to the Intoxin A receptor
6 FILE REFERENCE: 15,81,010
7 CURRENT APPLICATION NUMBER: 05-200-2408-572
8 CURRENT FILING DATE: 1999-08-04
9 EARLIER APPLICATION NUMBER: 05-08/914,042
10 EARLIER FILING DATE: 1997-08-05
11 NUMBER OF SEQ ID NOS: 47
12 SEQ ID NO: 27
13 SEQUENCE: WordPerfect 8.0
14 LENGTH: 8
15 TYPE: PRT
16 ORGANISM: Artificial Sequence
17 FEATURE:
18 OTHER INFORMATION: Exhibit 8 sequence similarity to a portion of human H1-2.
19 US-09-128-572-27

```

```

Query Match 35.0% Score 21: DB 4: Length 8:
Host Local Similarity 64.3%: Prod. No. 1.7e+05:
Matches 5: Conservative 0: Mismatches 1: Indels 0: Gaps 0:
UY 6 IMINKI 11
DB 1 IMINKI 6

```

```

RESULT 15
US-09-128-572-27
1 Patient No. 5204259
2 APPLICANT: HELLING, THOMAS B. CONEY, HAKAY, WERN,
3 MICHAEL F.
4 TITLE OF INVENTION: WITH 4-5 AND SYSTEMS FOR PREVENTING HIV
5 ANTIGENS
6 NUMBER OF SEQUENCES: 20

```

```

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: 05-200-2408-560
3 FILING DATE: 14 MAR 1995
4 CLASSIFICATION: 424
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 05-200-2408-560
7 FILING DATE: 14 MAR 1995
8 ATTORNEY/AGENT INFORMATION:
9 NAME: BARBIO, A USA A
10 REGISTRATION NUMBER: 44,895
11 REFERENCE: 211,002
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: (508) 359 3876
14 TELEFAX: (508) 359 3885
15 INFORMATION FOR SEQ ID NO: 470:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 8 amino acids
18 TYPE: amino acid
19 STRANDEDNESS: single
20 ORIENTATION: forward
21 MOLECULE TYPE: peptide
22 DS: 04 444 B18 470

```

```

Query Match 35.0% Score 21: DB 6: Length 8:
Host Local Similarity 50.0%: Prod. No. 1.7e+05:
Matches 3: Conservative 2: Mismatches 1: Indels 0: Gaps 0:
UY 2 HRAKTM 7
DB 3 HRAKTM 8

```

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Search completed: July 15, 2002, 14:06:27
Job time: 180 sec

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